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(54) Title: PROTEIN-PROTEIN FROM S. CEREVISIAE AND METHODS OF USING SAME			
(57) Abstract			
<p>The invention provides complexes of at least two polypeptides from the yeast <i>S. cerevisiae</i> and methods of using the same. Purified complexes of two polypeptides are provided, including chimeric complexes, and chimeric polypeptides and complexes thereof are also provided, as are nucleic acids encoding chimeric polypeptides and vectors and cells containing the same. Also provided are methods of identifying agents that disrupt polypeptide complexes, methods of identifying complex or polypeptide in a sample, and for removing the same, methods of determining altered expression of a polypeptide in a subject and methods of treating/preventing disorders involving altered levels of complex or polypeptide.</p>			

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PROTEIN-PROTEIN FROM *S. CEREVISIAE* AND METHODS OF USING SAME

## FIELD OF THE INVENTION

The invention relates generally to polypeptides and complexes of two or more  
5 polypeptides, as well as to methods of use thereof.

## BACKGROUND OF THE INVENTION

Most, if not all, biologically important activities are mediated at the tissue, cellular, and  
subcellular level at least in part by interactions between one or more proteins. These  
biologically important activities can include, e.g., cell division, cell differentiation, anabolic  
10 activities, and catabolic activities. Interacting proteins or polypeptides can form a complex.  
Accordingly, failure to form a given polypeptide complex can result in deleterious  
consequences to a cell or individual. Conversely, the inappropriate formation of a given  
polypeptide complex can likewise be undesirable.

15 The identification of protein complexes associated with specific biological activities  
can be used to identify or prevent conditions associated with the absence or presence of these  
complexes.

## SUMMARY OF THE INVENTION

The invention is based, in part, upon the identification of protein-protein interactions in  
the yeast *S. cerevisiae* and humans. Interacting proteins present in complexes according to the  
20 invention are shown in, e.g., Table 3.

In one aspect, the invention provides a purified complex including a first polypeptide  
that includes the amino acid sequence encoded by the open reading frame ("ORF") listed in  
Table 3, column 1, and a second polypeptide that includes the amino acid sequence of the  
corresponding polypeptide encoded by the ORF recited in column 5 of Table 3. Gene names  
25 for the ORFs recited in Table 3, column 1, and Table 3, column 5 are provided in Table 3,  
columns 2 and 6, respectively.

In another aspect, the invention provides a purified complex including a first  
polypeptide and a second polypeptide selected from, or including, the human polypeptides

recited in Table 7, column 2, and the corresponding polypeptides recited in Table 7, column 6. Complexes of polypeptides including the binding domains of such polypeptides, and complexes having labeled polypeptide, are also provided.

- The invention also provides purified complexes of a first and a second polypeptide.
- 5    The first polypeptide is a polypeptide functionally classified in the MIPS database as a Cell/Growth/Cell Division/DNA Synthesis protein; a Cell Rescue/Cell Defense/Cell Death and Aging Protein; a Cellular Biogenesis protein; a Cellular Organization protein; a Classification Not-Yet Clear Cut protein; an Energy Protein; an Intracellular Transport protein; an Ionic Homeostasis protein, a Metabolism protein; a Protein Destination protein; a Protein Synthesis protein; a Retrotransposon/Plasmid protein; a Signal Transduction protein; a Transcription protein; a Transport Facilitation protein, or an Unclassified protein. The second polypeptide is the corresponding polypeptide recited in Table 3, column 5 or Table 7, column 6, respectively.
- 10
- 15

The invention also provides a purified complex of a first and second polypeptide, where at least one of the polypeptides is a microtubule or microtubule-associated protein, a heme biosynthesis protein, or a cell wall or cell-wall synthesis protein.

The invention further provides purified chimeric complexes including a yeast polypeptide and a human ortholog polypeptide. In some embodiments the yeast polypeptide includes the amino acid sequence of the polypeptides recited in Table 7, column 1, and the human polypeptide includes the amino acid sequence of the corresponding polypeptides recited in Table 7, column 6. In other embodiments the yeast polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 5, and the human ortholog polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 2.

In a further aspect, the invention provides chimeric polypeptides having six or more amino acids of a first polypeptide covalently linked to six or more amino acids of a second polypeptide. In some embodiments, the chimeric polypeptides are yeast-yeast chimeras, while in others the chimeric polypeptides are human-human or yeast-human chimera. In some embodiments, the first polypeptide is selected from the polypeptides recited in Table 3, column 1, and the second polypeptide is selected from the polypeptides recited in Table 3, column 5. In other embodiments, the first polypeptide is selected from polypeptides recited in Table 7, columns 1 or 2, and the second polypeptide is selected from the polypeptides recited in Table 7, columns 5 or 6. Nucleic acids encoding chimeric polypeptides, and vectors and cells containing the same, are also provided.

In yet another aspect, the invention provides an antibody which specifically binds polypeptide complexes according to the invention. The antibody preferably binds to a complex comprising one or more polypeptides with greater affinity than its affinity for either polypeptide that is not present in the complex.

5 Also provided by the invention are kits containing reagent which can specifically detect the complexes of the invention. In one embodiment, the reagent is a complex-specific antibody, while in other embodiments the reagent is an antibody specific for the first or second polypeptides of the complex.

10 In another aspect, the invention provides pharmaceutical compositions including the complexes described herein. Such compositions are formulated to be suitable for therapeutic administration in the treatment of deficiencies or diseases involving altered levels of the complexes of the invention.

15 In still another aspect, the invention provides methods of identifying an agent which disrupts a polypeptide complex by providing a complex described herein, contacting the complex with a test agent, and detecting the presence of a polypeptide displaced from the complex. In certain embodiments, the complex includes at least one polypeptide comprising a microtubule or microtubule-associated protein, a heme biosynthesis protein, or a cell wall or cell-wall synthesis protein.

20 In a further aspect, the invention provides a method for inhibiting the interaction of a protein with a ligand by contacting a complex of the protein and ligand with an agent that disrupts the complex. In certain embodiments, the protein is a microtubule or microtubule associated protein, a heme biosynthesis protein, or a cell wall or cell-wall synthesis protein, and the ligand is a corresponding interacting polypeptide described herein.

25 In yet another aspect, the invention provides a method of identifying a polypeptide complex in a subject by providing a biological sample from the subject and detecting, if present, the level of a complex, described herein, in the subject.

Also provided by the invention is a method for detecting a polypeptide in a biological sample by providing a biological sample containing a first polypeptide, and contacting the sample with a second polypeptide under conditions suitable to form a polypeptide complex.

30 In another aspect, the invention provides a method for removing a first polypeptide from a biological sample by providing a biological sample including the first polypeptide, contacting the sample with a second polypeptide under conditions suitable for formation of a

polypeptide complex, and removing the complex, thereby effectively removing the first polypeptide. In certain embodiments, the first polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 2, and the second polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 6. In another embodiment, the first 5 polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 6, and the second polypeptide is selected from, or includes, the polypeptides recited in Table 7, column 2.

In a further aspect, the invention provides a method for determining altered expression of a polypeptide in a subject by providing a biological sample from the subject, measuring the 10 level of polypeptide complex in the sample, and comparing the level of the complex in the sample to the level of complex in a reference sample with a known polypeptide expression level.

In a still further aspect, the invention provides a method of treating or preventing a disease or disorder involving altered levels of a complex described herein or a polypeptide 15 described herein, by administering, to a subject in need thereof, a therapeutically-effective amount of at least one molecule that modulates the function of the complex or polypeptide. In one embodiment, the agent modulates the function of a polypeptide selected from the polypeptides recited in Table 7, columns 2 or 6.

In the specification and the appended claims, the singular forms include plural referents unless the context clearly dictates otherwise. Unless defined otherwise, all technical 20 and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. All patents and publications cited in this specification are incorporated by reference herein in their entirety.

#### DETAILED DESCRIPTION OF THE INVENTION

The invention provides complexes of interacting polypeptides which have not 25 heretofore been shown to interact directly, as well as methods of using these complexes.

Some interacting polypeptides were identified by identifying which of the predicted open-reading frames (ORFs) of the yeast *S. cerevisiae* encode polypeptides that interact in a yeast two-hybrid system. In one screen, 692 discrete interacting protein pairs were discovered. 30 These interacting pairs include (i) interactions that place functionally unclassified proteins in a biological context, (ii) novel interactions between proteins involved in the same biological function, and (iii) novel interactions that link together biological functions into larger cellular

processes.

A summary of the screening used to identify interacting yeast ORFs is shown in Table 1.

Table 1: Screen Summary

5

	Description	Total
10	Yeast ORF PCR Products	6144
	Yeast ORFs cloned <sup>a</sup>	5345
	ORFs pooled to generate the activation domain library	5341 <sup>b</sup>
	Yeast ORFs identified to have interactions <sup>c</sup>	817
15	Total discrete interacting protein pairs	692
	Interactions identified in independent experiments <sup>d</sup>	286
	Interactions identified multiple times in a single experiment	186
	Interactions identified only once	220

20 <sup>a</sup>Number of PCR products giving transformants in both plasmids (pOBD2 and pOAD).

<sup>b</sup>One yeast ORF activation domain construct was excluded from the pool due to self-activation in a test screen (YJR009C - glyceraldehyde-3-phosphate dehydrogenase and YNL333W - Snz2) and three yeast ORF activation domain constructs were excluded because they encoded proteins that could affect the selection process (YPL248C – Gal4, YML051W – Gal80 and YEL021W – Ura3).

25 <sup>c</sup>The total number of yeast ORFs found as an interacting binding domain clone and/or an interacting activation domain clone in the screens.

<sup>d</sup>All screening experiments were performed in duplicate.

Table 2 indicates that the interacting proteins disclosed herein can be grouped by functional roles using the Munich Information Center for Protein Sequences ("MIPS") classification system.

5 Table 2: Interactions grouped by Protein Functional Roles (as classified by the MIPS database)<sup>a</sup>

	MIPS Classification	MIPS	Results from the screen			
		Classification	Proteins in Category <sup>b</sup>	Proteins with Interactions <sup>c</sup>	Total Interactions	Interactions within a Category
10	MIPS classification					
	Metabolism	1023	133	189	40	
	Energy	239	29	39	3	
15	Cell Growth, Cell Division and DNA Synthesis	767	138	227	46	
	Transcription	734	134	183	38	
	Protein Synthesis	345	18	37	5	
	Protein Destination	525	76	98	15	
20	Transport Facilitation	302	14	20	0	
	Intracellular Transport	438	50	99	8	
	Cellular Biogenesis	185	23	35	3	
	Signal Transduction	122	25	32	4	
	Cell Rescue, Defense, Cell Death and Aging	341	48	69	7	
25	Ionic Homeostasis	120	8	18	0	
	Cellular Organization	2144	290	388	130	
	Retrotransposons and Plasmid Proteins <sup>d</sup>	113	1	1	0	
30	Classification Not Yet Clear-Cut	151	22	42	1	
	Unclassified Proteins	2593	313	388	110	

<sup>a</sup>In the MIPS database, proteins have been classified into at least one category, and one third of proteins have been placed in more than one category. See MIPS Yeast Genome Database (MYGD) Functional Catalogue, [www.mips.biochem.mpg.de/proj/yeast](http://www.mips.biochem.mpg.de/proj/yeast); Mewes *et al.*, Nucl. Acid. Res. 25: 28 (1997); Mewes *et al.*, Nucl. Acid. Res. 26: 33 (1998).

<sup>b</sup>Numbers based on 6234 ORFs.

<sup>c</sup>Total based on 885 ORFs. Total interactions with at least one protein in the category.

<sup>d</sup>Only eight of the yeast ORFs in this category were contained in the original 6144 ORF screening population.

Some newly disclosed interactions place functionally unclassified proteins from the yeast genome in a biological context. For example, two proteins of unknown function, YGR010Wp and YLR328Wp (77% identical), were observed to interact with each other, and also to bind to ornithine aminotransferase (Car2p), which catalyzes a step in arginine metabolism. This observation suggests that YGRO10WP and YLR328Wp are implicated in arginine metabolism. In addition, because YGR010Wp and YLR328Wp are 40% identical to the human protein KIAA0479 (Genbank accession number AB007948), the interactive data further suggest tha the human protein KIAA0479 is also involved in arginine metabolism.

Also included in the interactions are complexes of two or more proteins involved in functional pathways for which direct interactions have not been described previously. For example, proteins involved in autophagy, e.g., Apg13p, are shown herein to interact with proteins of the Cvt (cytoplasm-to-vacuole targeting) pathway, e.g., Lap4p. Previously, direct interactions between proteins involved in autophagy and the Cvt pathway had not been reported. Autophagy is a degradation pathway used under conditions of nutrient stress to non-selectively recycle cytoplasmic proteins and organelles to their constituent components, while the Cvt pathway is a biosynthetic pathway that transports the vacuolar enzyme aminopeptidase I (API, encoded by *LAP4*) specifically to the vacuole. See Scott *et al.*, *Curr. Opin. Cell. Biol.* 10: 523 (1998). Several mutants in the Cvt pathway (*cvt*) and autophagocytosis (*aut* and *apg*) are allelic, suggesting that both pathways utilize some of the same molecular components. See Tsukada *et al.*, *FEBS Letters* 333: 169 (1993); Thumm *et al.*, *FEBS Letters* 349: 275 (1994); Harding *et al.*, *J. Cell. Biol.* 131: 17621 (1996); Scott *et al.*, *Proc. Natl. Acad. Sci. USA* 93: 12304 (1996).

A number of ORFs encoding proteins of unknown functions have been identified as components of autophagy. Since several of the genes altered in *apg*, *aut*, and *cvt* mutants have not yet been cloned, ORFs found in these interactions can be examined to determine if they encode any of these altered genes. It has also been shown that Lap4p is a self-interactor, corroborating previous evidence that Lap4p assembles into a dodecamer (see Funakoshi *et al.*, *Gene* 192: 207 (1997)), and the observed interaction between Apg1 and Apg13 lends support to previous genetic evidence suggesting that *APG1* is a high-copy suppressor of *apg13* (Kim *et al.*, *J. Cell. Biol.* 137: 609 (1997)).

An interaction was also identified between YDR201Wp and YKR037Cp, two proteins known to be localized to the spindle pole body by mass spectrometry. See Wigge *et al.*, *J. Cell Biol.* 141: 967 (1998). The interaction of these proteins may indicate their involvement in the regulation of mitotic events.

New insights into novel interactions between proteins involved in the same biological function are also provided. For example, the nuclear polyadenylated RNA-binding proteins Nab2p and Nab4p bind to the 3' end of mRNA, but have distinct roles. See Kessler *et al.*, *Genes Dev.* 11: 2545 (1997). Nab2p is required for the regulation of poly(A) tail length and export of mRNA from the nucleus, and Nab4p is essential for the cleavage of pre-mRNA at the correct 3' site. The newly described interaction between Nab2p and Nab4p suggests that they may act in concert.

Similarly, in yeast, diverse cyclins bind to Cdc28p in a coordinated manner to modulate its kinase activity during the cell cycle. The B-type cyclins play a critical role in the induction of bipolar mitotic spindle formation. See Nasmyth, *Curr. Opin. Cell. Biol.* 5: 166 (1993). Each of the B-type cyclins, Clb1p, Clb2p and Clb3p, has presently been observed to 5 form a complex with Cks1p and Cdc28p. The identification of interactions between Cks1p and each of Clb1p, Clb2p and Clb3p, suggests that the kinase activity of Cdc28p could be mediated by cyclin Bs through their interaction with Cks1p.

In another example, Ypt53p, a rab5-like GTPase involved in vacuolar protein sorting and endocytosis, has presently been shown to interact with Siw4p, a putative tyrosine 10 phosphatase which acts in a complex to control nutrient-dependent cell proliferation. See Singer-Kruger *et al.*, *J. Cell. Biol.* 125: 283 (1994); Saul *et al.*, *Gen. Microbiol.* 131: 1797 (1985). One possible explanation for the observed interaction is that Ypt53p senses nutrient 15 availability to coordinate cell cycle progression.

The newly identified protein-protein interactions connect biological functions into 15 larger cellular processes. For example, the nuclear pore complex (NPC), consisting of as many as 50 different subunits, is the macromolecular-conducting channel between the nucleus and the cytoplasm. See Fabre *et al.*, *Ann. Rev. Genet.* 31: 277 (1997); Marelli *et al.*, *J. Cell Biol.* 143: 1813 (1998). Two newly identified NPC components, Nup53p and Nup59p/Asm4p, interact with Ndc1p, a protein required for spindle pole body (SPB) 20 duplication and component of the nuclear envelope. Evidence of a physical interaction between components of the NPC and SPB suggests that these two structures located in the nuclear envelope may coordinate communication between the nucleus and the cytoplasm.

Another interaction involves the meiosis-specific protein, Msh5p, which is required for the resolution of cross-overs during meiosis. Hollingsworth *et al.*, *Genes Dev.* 9: 1728 (1995). 25 Meiotic recombination is initiated by double-strand breaks (DSBs), a prerequisite to cross-over formation that is resolved in a structure called the synaptonemal complex (SC). Mre11p is part of a complex that participates in DSB formation. See Usui *et al.*, *Cell* 95: 705 (1998). It is also known that Tid3p helps form the spindle pole body and interacts with Dmc1p, a 30 protein required for the formation of the SC. See Bishop *et al.*, *Cell* 69: 439-56 (1992). It has presently been shown that Msh5p interacts with both Mre11p and Tid3p. These novel associations tie DSB formation and the resolution of cross-overs with Msh5p as the linking protein.

Similarly, to exit the cell cycle, cells must undergo a series of checkpoints that monitor correct microtubule and spindle formation. See Guenette *et al.*, *J. Cell. Sci.* 108: 195 (1995). The present invention identifies at least two interactions that tie cycle regulation to microtubule assembly. The first is between a microtubule checkpoint protein, Bub3p and a 5 spindle pole body checkpoint protein, Mad3p. This observation mirrors the recent interaction described between the human homologs of Bub3p and Mad3p. See Hoyt *et al.*, *Cell* 66: 507-17 (1991); Hwang *et al.*, *Science* 279: 1041 (1998); Taylor *et al.*, *J. Cell Biol.* 142: 1 (1998). Interestingly, the second is between Mad3p and a known regulator of the Cdc28p 10 kinase, Cln3p, See Cvrckova *et al.*, *EMBO J.* 12: 5277 (1993). These interactions could give rise to a cascade Bub3→Mad3→Cln3p→Cdc28p, and may suggest a pathway to propagate the signal of incorrect microtubule formation during early events at the cell cycle arrest in G1 phase.

The complexes disclosed herein are useful, *inter alia*, in identifying agents which modulate cellular processes in which one or more members of the complex have previously 15 been associated. For example, interacting Pro-Pairs 1a-1b (representing open reading frames YGR108W and YBR135W, or genes CLB1 and CKS1, respectively) as shown in Table 3, have both been previously implicated in cell growth, cell division, and /or DNA synthesis. Accordingly, new agents which modulate cell growth, cell division, and/or DNA synthesis can 20 be identified by evaluating the ability of a test agent to affect formation or dissolution of a complex of the Pro-Pairs 1a and 1b.

Complexes according to the invention can also be used in methods for identifying a desired polypeptides in a biological sample by forming a complex of a first polypeptide and a second polypeptide that interacts with the first polypeptide. The presence of the complex indicates that the sample contains the first polypeptide.

25 These utilities, as well as additional utilities, are discussed in greater detail below

### Purified Polypeptide Complexes

In one aspect, the invention includes a purified complex that includes two or more polypeptides. In one embodiment, the invention provides purified complexes of two or more polypeptides. One of the polypeptides includes a polypeptide selected from the polypeptides 30 recited in Table 3, column 1 (referenced as ProPair 1a-692a) and another includes a polypeptide selected from the polypeptides recited in Table 3, column 5 (referenced as ProPair 1b-692b). In some embodiments the first and second polypeptides of the complex are the

polypeptides enumerated in Table 3. In some embodiments a first polypeptide is listed as a "bait" polypeptide and a second polypeptide is denoted as "prey" polypeptide, while in other embodiments the first polypeptide corresponds to a "prey" polypeptide and the second is a "bait" polypeptide.

5 By "corresponding polypeptide" is meant, with reference to Tables 3-7, the polypeptide recited in the same row, reading across from left-to-right or right-to-left, as a specific selected peptide. For example, in Table 3, in the first row, the corresponding polypeptide of YGR108W is YBR135W. These protein pairs are designated as 1a and 1b, as is indicated in Table 3.

10 Similarly, in the first row, the corresponding polypeptide of YBR135W (ProPair 1b) is YBR108W (ProPair 1a). In the second row, however, the corresponding polypeptide of YBR135W (a prey protein; ProPair 2b) is YPR119W (a bait protein; ProPair 2a).

15 Also as used herein, "protein" and "protein complex" are used synonymously with "polypeptide" and "polypeptide complex." A "purified" polypeptide, protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the polypeptide is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of polypeptide complex having less than about 30% (by dry weight) of non-complex proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of contaminating protein, still more preferably less than about 10% of contaminating protein, and most preferably less than about 5% non-complex protein. When 20 the polypeptide or complex is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

Table 3. Protein Pairs Identified in the Screen.

Binding Domain Fusion "Bait"	Binding Domain Fusion	Pro-Pair Ref. No. (MIPS)	Functional Classification	Activation Domain Fusion "Prey"	Activation Domain Ref. No. (MIPS)	Functional Classification
[ORF] YGR108W	[Gene] CLB1	1a	Cell Growth; Cell Division And DNA Synthesis;	[ORF] YBR135W	1b	Cell Growth; Cell Division And DNA Synthesis;
YPR119W	CLB2	2a	Cell Growth; Cell Division And DNA Synthesis;	YBR135W	CKS1	Cell Growth; Cell Division And DNA Synthesis;
YDL155W	CLB3	3a	Cell Growth; Cell Division And DNA Synthesis;	YBR135W	CKS1	Cell Growth; Cell Division And DNA Synthesis;
YDR206W	EBS1	4a	Cell Growth; Cell Division And DNA Synthesis;	YJL030W	MAD2	Cell Growth; Cell Division And DNA Synthesis;
YDR206W	EBS1	5a	Cell Growth; Cell Division And DNA Synthesis;	YBR057C	MUM2	Cell Growth; Cell Division And DNA Synthesis;
YGL175C	SAE2	6a	Cell Growth; Cell Division And DNA Synthesis;	YGL175C	SAE2	Cell Growth; Cell Division And DNA Synthesis;
YGL229C	SAP4	7a	Cell Growth; Cell Division And DNA Synthesis;	YJL030W	MAD2	Cell Growth; Cell Division And DNA Synthesis;
YOR026W	BUB3	8a	Cell Growth; Cell Division And DNA Synthesis;	YJL013C	MAD3	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
YGL229C	SAP4	9a	Cell Growth; Cell Division And DNA Synthesis;	YJL013C	MAD3	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
YDL127W	PCL2	10a	Cell Growth; Cell Division And DNA Synthesis;	YDR146C	SWI5	Cell Growth; Cell Division And DNA Synthesis; Transcription;
YDR108W	GSG1	11a	Cell Growth; Cell Division And DNA Synthesis;	YGR234W	YHB1	Cellular Organization; Cell Death And Aging; Cellular Organization;
YDR099W	BMH2	12a	Cell Growth; Cell Division And DNA Synthesis;	YBL043W	ECM13	Cellular Biogenesis;
YOL034W		13a	Cell Growth; Cell Division And DNA Synthesis;	YMR117C		Cellular Organization;
YER180C	ISC10	14a	Cell Growth; Cell Division And DNA Synthesis;	YGL026C	TRP5	Metabolism; Cellular Organization;
YGL229C	SAP4	15a	Cell Growth; Cell Division And DNA Synthesis;	YBR196C	PG11	Metabolism; Energy; Cellular Organization;
YGL155W	RCK1	16a	Cell Growth; Cell Division And DNA Synthesis;	YLR113W	HOG1	Metabolism; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;

YDR206W	EBS1	17a	Cell Growth, Cell Division And DNA Synthesis;	YER027C	GAL83	17b	Metabolism; Transcription;
YDR206W	EBS1	18a	Cell Growth, Cell Division And DNA Synthesis;	YOR047C	STD1	18b	Metabolism; Transcription;
YPR119W	CLB2	19a	Cell Growth, Cell Division And DNA Synthesis;	YNL135C	FPR1	19b	Protein Destination; Cellular Organization; Transcription;
YDR206W	EBS1	20a	Cell Growth, Cell Division And DNA Synthesis;	YOL149W	DCP1	20b	
YLR117C	SYF3	21a	Cell Growth, Cell Division And DNA Synthesis;	YBR188C	NTC20	21b	Transcription;
YFL035C	MOB2	22a	Cell Growth, Cell Division And DNA Synthesis;	YOL036W		22b	Unclassified Proteins;
YDR099W	BMH2	23a	Cell Growth, Cell Division And DNA Synthesis;	YNL042W		23b	Unclassified Proteins;
YPR119W	CLB2	24a	Cell Growth, Cell Division And DNA Synthesis;	YDR386W	MUS81	24b	Unclassified Proteins;
YPR119W	CLB2	25a	Cell Growth, Cell Division And DNA Synthesis;	YDR412W		25b	Unclassified Proteins;
YPR119W	CLB2	26a	Cell Growth, Cell Division And DNA Synthesis;	YHR035W		26b	Unclassified Proteins;
YPR119W	CLB2	27a	Cell Growth, Cell Division And DNA Synthesis;	YNR022C		27b	Unclassified Proteins;
YPR046W	MCM16	28a	Cell Growth, Cell Division And DNA Synthesis;	YJR135C	MCM22	28b	Unclassified Proteins;
YOR127W	RGA1	29a	Cell Growth, Cell Division And DNA Synthesis;	YHL042W		29b	Unclassified Proteins;
YOR127W	RGA1	30a	Cell Growth, Cell Division And DNA Synthesis;	YJL185C		30b	Unclassified Proteins;
YGL175C	SAE2	31a	Cell Growth, Cell Division And DNA Synthesis;	YCR086W		31b	Unclassified Proteins;
YGL229C	SAP4	32a	Cell Growth, Cell Division And DNA Synthesis;	YJL178C		32b	Unclassified Proteins;
YGL229C	SAP4	33a	Cell Growth, Cell Division And DNA Synthesis;	YJL211C		33b	Unclassified Proteins;
YGL229C	SAP4	34a	Cell Growth, Cell Division And DNA Synthesis;	YMR181C		34b	Unclassified Proteins;
YGL229C	SAP4	35a	Cell Growth, Cell Division And DNA Synthesis;	YOR062C		35b	Unclassified Proteins;
YGL229C	SAP4	36a	Cell Growth, Cell Division And DNA Synthesis;	YPR040W		36b	Unclassified Proteins;
YMR096W	SNZ1	37a	Cell Growth, Cell Division And DNA Synthesis;	YMR095C	SNO1	37b	Unclassified Proteins;
YHR014W	SPO13	38a	Cell Growth, Cell Division And DNA Synthesis;	YHR185C		38b	Unclassified Proteins;
YLR215C		39a	Cell Growth, Cell Division And DNA Synthesis;	YLR386W		39b	Unclassified Proteins;

YDR076W	RAD55	40a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER095W	RAD51	40b	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YOR368W	RAD17	41a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging;	YLR288C	MEC3	41b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging; Unclassified Proteins;
YPL204W	HRR25	42a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YHR185C		42b	
YJL160C		43a	Cell Growth, Cell Division And DNA Synthesis; Cell Rescue, Defense, Cell Death And Aging; Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;	YCR059C		43b	Unclassified Proteins;
YPL140C	MKK2	44a	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;	YHR030C	SLT2	44b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;
YLR288C	MEC3	45a	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging; Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YMR159C	SAP18	45b	Unclassified Proteins;
YGR014W	MSB2	46a	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging; Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL030W	MAD2	46b	Cell Growth, Cell Division And DNA Synthesis;
YDL154W	MSH5	47a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YBR133C	HSL7	47b	Cell Growth, Cell Division And DNA Synthesis;
YDL154W	MSH5	48a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YMR224C	MRE11	48b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YAL040C	CLN3	49a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL013C	MAD3	49b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YPL049C	DIG1	50a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDR480W	DIG2	50b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YER179W	DMC1	51a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YER179W	DMC1	51b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YIL150C	DNA43	52a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL201C	MCM6	52b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;

YGR014W	MSB2	53a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL013C	MAD3	53b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YHR184W	SSP1	54a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YHR184W	SSP1	54b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDR388W	RVS167	55a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YCR009C	RVS161	55b	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;
YGR014W	MSB2	56a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDL165W	CDC36	56b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YDL154W	MSH5	57a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL025C	PGD1	57b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YMR139W	RIM11	58a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJR094C	IME1	58b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization; Cell Rescue, Defense, Cell Death And Aging;
YML031W	NDC1	59a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDL088C	ASM4	59b	Cellular Organization;
YDL017W	CDC7	60a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGR099W	TEL2	60b	Cellular Organization;
YGR014W	MSB2	61a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YIL144W	TID3	61b	Cellular Organization;
YDL154W	MSH5	62a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YIL144W	TID3	62b	Cellular Organization;
YDL017W	CDC7	63a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YKL039W	PTM1	63b	Classification Not Yet Clear-Cut;
YOL069W	NUF2	64a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YER099C	PRS2	64b	Metabolism;
YDR218C	SPR28	65a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJR076C	CDC11	65b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDL017W	CDC7	66a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YJL088W	ARG3	66b	Metabolism; Cellular Organization;
YDL017W	CDC7	67a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YDL160C	DHH1	67b	Transcription; Cellular Organization;
YGR014W	MSB2	68a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YPL211W	NIP7	68b	Transcription; Cellular Organization;

YLR319C	BUD6	69a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL015C	69b	Unclassified Proteins;		
YDL017W	CDC7	70a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YCR022C	70b	Unclassified Proteins;		
YDL017W	CDC7	71a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YCR050C	71b	Unclassified Proteins;		
YDL017W	CDC7	72a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YEL023C	72b	Unclassified Proteins;		
YDL017W	CDC7	73a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YFR057W	73b	Unclassified Proteins;		
YDL017W	CDC7	74a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YNR048W	74b	Unclassified Proteins;		
YDL017W	CDC7	75a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YOR006C	75b	Unclassified Proteins;		
YDL154W	MSH5	76a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YGL170C	76b	Unclassified Proteins;		
-	YML031W	NDC1	77a	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	YMR153W	77b	Unclassified Proteins;	
-	YNL189W	SRP1	78a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YKL130C	SHE2	78b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YDR335W	MSN5	79a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport;	YDR146C	SWI5	79b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	
YNL189W	SRP1	80a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YML028W	TSA1	80b	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	
YNL154C	YCK2	82a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YMR226C		81b	Classification Not Yet Clear-Cut;	
YNL189W	SRP1	83a	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;	YOR355W	GDS1	82b	Classification Not Yet Clear-Cut;	
				YBR252W	DUT1	83b	Metabolism;	





YPR054W	SMK1	109a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YFL029C	CAK1	109b	Cell Growth, Cell Division And DNA Synthesis;
YLR229C	CDC42	110a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;	YDL135C	RDI1	110b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;
YLR362W	STE11	111a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YCL032W	STE50	111b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;
YJR086W	STE18	112a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;	YOR212W	STE4	112b	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction; Cellular Organization;
YLR305C	STT4	113a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YOR355W	GDS1	113b	Classification Not Yet Clear-Cut;
YLR305C	STT4	114a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YOR047C	STD1	114b	Metabolism; Transcription;
-	YMR052W	FAR3	115a	Cell Growth, Cell Division And DNA Synthesis; Signal Transduction;	YFR008W	115b	Unclassified Proteins;
-	YAR003W	116a	Cell Growth, Cell Division And DNA Synthesis; Transcription;	YBR175W		116b	Unclassified Proteins;
-	YAR003W	117a	Cell Growth, Cell Division And DNA Synthesis; Transcription;	YDR140W		117b	Unclassified Proteins;
YGL192W	IME4	118a	Cell Growth, Cell Division And DNA Synthesis; Transcription;	YBR057C	MUM2	118b	Cell Growth, Cell Division And DNA Synthesis;
YCL055W	KAR4	119a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YBR057C	MUM2	119b	Cell Growth, Cell Division And DNA Synthesis;
YNL210W	MER1	120a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YKL142W	MRP8	120b	Protein Synthesis; Cellular Organization;
YOR061W	CKA2	121a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOR039W	CKB2	121b	Transcription; Cellular Organization;
YNR010W	CSE2	122a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOR174W	MED4	122b	Transcription; Cellular Organization;
YHL027W	RIM101	123a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YJL056C	ZAP1	123b	Transcription; Cellular Organization;
YOL006C	TOP1	124a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YMR233W		124b	Unclassified Proteins;

YLR33C	CNA1	125a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Ionic Homeostasis; Cellular Organization;	YNL047C	125b	Unclassified Proteins;
YGL058W	RAD6	126a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YCR066W	126b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YPR018W	RLF2	127a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Protein Destination; Cellular Organization;	YBR195C	127b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Protein Destination; Cellular Biogenesis; Signal Transduction; Cellular Organization;
YHR084W	STE12	128a	Cell Growth, Cell Division And DNA Synthesis; Transcription; Signal Transduction; Cellular Organization;	YDR480W	128b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YBR244W		129a	Cell Rescue, Defense, Cell Death And Aging;	YLR117C	129b	Cell Growth, Cell Division And DNA Synthesis;
YLL057C		130a	Cell Rescue, Defense, Cell Death And Aging;	YLL057C	130b	Cell Rescue, Defense, Cell Death And Aging;
YIL011W		131a	Cell Rescue, Defense, Cell Death And Aging;	YMR201C	131b	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YHL046C		132a	Cell Rescue, Defense, Cell Death And Aging;	YOR355W	132b	Classification Not Yet Clear-Cut;
YGR213C	RTA1	133a	Cell Rescue, Defense, Cell Death And Aging;	YHR134W	133b	Unclassified Proteins;
YDR061W		134a	Cell Rescue, Defense, Cell Death And Aging;	YCR086W	134b	Unclassified Proteins;
YLR046C		135a	Cell Rescue, Defense, Cell Death And Aging;	YHL006C	135b	Unclassified Proteins;
YJL092W	HPR5	136a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YOR355W	136b	Classification Not Yet Clear-Cut;
YDR077W	SED1	137a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	HEM13	137b	Metabolism; Cellular Organization;
YJL092W	HPR5	138a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YDR044W	138b	Protein Destination;
YJL092W	HPR5	139a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YBR184W	139b	Unclassified Proteins;
YJL092W	HPR5	140a	Cell Rescue, Defense, Cell Death And Aging; Cellular Organization; Cellular Biogenesis; Cellular Organization;	YDR078C	140b	Unclassified Proteins;
YLR390W	ECM19	141a	Cellular Biogenesis; Cellular Organization;	YDR145W	141b	Transcription;
YHR17W		142a	Cellular Biogenesis; Cellular Organization;	YBR217W	142b	Protein Destination; Cellular Biogenesis; Cellular Organization;
YHR17W		143a	Cellular Biogenesis; Cellular Organization;	YNR007C	143b	Protein Destination; Intracellular Transport;

	YHR171W	144a	Cellular Biogenesis; Cellular Organization;	YBL078C	AUT7	144b	Protein Destabilization; Intracellular Transport; Cellular Organization;	
	YKR037C	145a	Cellular Organization;	YJR091C	JSN1	145b	Cell Growth, Cell Division And DNA Synthesis;	
	YCL059C	KRR1	146a	Cellular Organization;	YGL201C	MCM6	146b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
	YDR106W	ARP10	147a	Cellular Organization;	YHR129C	ARP1	147b	Cell Growth, Cell Division And DNA Synthesis; Intracellular Transport; Cellular Organization;
	YMR092C	AlP1	148a	Cellular Organization;	YLR102C	APC9	148b	Cell Growth, Cell Division And DNA Synthesis; Protein Destabilization;
	YDR201W		149a	Cellular Organization;	YIL144W	TID3	149b	Cellular Organization;
	YER018C		150a	Cellular Organization;	YMR117C		150b	Cellular Organization;
	YKR037C		151a	Cellular Organization;	YDR201W		151b	Cellular Organization;
	YLR429W	CRN1	152a	Cellular Organization;	YDR328C	SKP1	152b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destabilization; Cellular Organization;
	YER018C		153a	Cellular Organization;	YHR193C	EGD2	153b	Metabolism; Transcription;
-	YDR122W	KIN1	154a	Cellular Organization; Classification Not Yet Clear-Cut;	YOL082W		154b	Cellular Organization; Unclassified Proteins;
20	YNL218W		155a	Classification Not Yet Clear-Cut;	YJL030W	MAD2	155b	Cell Growth, Cell Division And DNA Synthesis;
-	YNL023C	FAP1	156a	Classification Not Yet Clear-Cut;	YMR224C	MRE11	156b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis; Cell Rescue, Defense, Cell Death And Aging;
	YNL023C	FAP1	157a	Classification Not Yet Clear-Cut;	YKL130C	SHE2	157b	Cellular Organization;
							Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	
	YCL024W		158a	Classification Not Yet Clear-Cut;	YKR048C	NAP1	158b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis; Cellular Organization;
	YFR024C-A		159a	Classification Not Yet Clear-Cut;	YBL007C	SLA1	159b	Cell Growth, Cell Division And DNA Synthesis; Protein Destabilization; Cellular Organization;
	YNL218W		160a	Classification Not Yet Clear-Cut;	YNL218W		160b	Classification Not Yet Clear-Cut;
	YLL046C	RNP1	161a	Classification Not Yet Clear-Cut;	YFR047C		161b	Metabolism;
	YBR274W		162a	Classification Not Yet Clear-Cut;	YLR238W	GSY2	162b	Metabolism; Energy; Cellular Organization;
	YDL002C	NHP10	163a	Classification Not Yet Clear-Cut;	YER092W		163b	Unclassified Proteins;
	YER059W	PC16	164a	Classification Not Yet Clear-Cut;	YJL084C		164b	Unclassified Proteins;

YER059W	PCL6	165a	Classification Not Yet Clear-Cut;	YLR190W	Unclassified Proteins;
YBR274W		166a	Classification Not Yet Clear-Cut;	YMR255W	Unclassified Proteins;
YDR084C		167a	Classification Not Yet Clear-Cut;	YGL161C	Unclassified Proteins;
YDR084C		168a	Classification Not Yet Clear-Cut;	YGL198W	Unclassified Proteins;
YFR024C-A		169a	Classification Not Yet Clear-Cut;	YGR268C	Unclassified Proteins;
YMR077C		170a	Classification Not Yet Clear-Cut;	YKL052C	Unclassified Proteins;
YHR039C		171a	Energy;	YDR480W	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YPR046W		172a	Energy;	YOR355W	Classification Not Yet Clear-Cut; Metabolism; Cellular Organization;
YPR046W		173a	Energy;	YDL215C	Metabolism; Transcription; Cellular Organization;
YPR048W		174a	Energy;	YNL199C	Metabolism; Transcription; Cellular Organization;
YNL118C	PSU1	175a	Energy;	YOL149W	Metabolism; Transcription; Cellular Organization;
YNL118C	PSU1	176a	Energy;	YEL015W	Metabolism; Transcription; Cellular Organization;
YPR048W	NIP100	177a	Energy;	YPR070W	Metabolism; Transcription; Cellular Organization;
YPL174C	NIP100	178a	Intracellular Transport;	YHR129C	Metabolism; Transcription; Cellular Organization;
YPL174C	NIP100	179a	Intracellular Transport;	YIL144W	Cellular Organization; Intracellular Transport; Cellular Organization;
YGR057C	LST7	180a	Intracellular Transport;	YKL015W	Cellular Organization; Intracellular Transport; Cellular Organization;
YPL174C	NIP100	181a	Intracellular Transport;	YIL184W	Cellular Organization; Intracellular Transport; Cellular Organization;
YER105C	NUP157	182a	Intracellular Transport; Cellular Organization;	YJL030W	Cellular Organization; Intracellular Transport; Cellular Organization;
YFR002W	NC96	183a	Intracellular Transport; Cellular Organization;	YGR120C	Cellular Organization; Intracellular Transport; Cellular Organization;
YHL019C	APM2	184a	Intracellular Transport; Cellular Organization;	YKL135C	Cellular Organization; Intracellular Transport; Cellular Organization;
YGR119C	NUP57	185a	Intracellular Transport; Cellular Organization;	YMR236W	Cellular Organization; Intracellular Transport; Cellular Organization;
YGR119C	NUP57	186a	Intracellular Transport; Cellular Organization;	YJL041W	Cellular Organization; Intracellular Transport; Cellular Organization;
YGR119C	NUP57	187a	Intracellular Transport; Cellular Organization;	YGL172W	Cellular Organization; Intracellular Transport; Cellular Organization;
YFR002W	NC96	188a	Intracellular Transport; Cellular Organization;	YMR153W	Cellular Organization; Intracellular Transport; Cellular Organization;
YER105C	NUP157	189a	Intracellular Transport; Cellular Organization;	YEL015W	Cellular Organization; Intracellular Transport; Cellular Organization;
YER105C	NUP157	190a	Intracellular Transport; Cellular Organization;	YMR153W	Cellular Organization; Intracellular Transport; Cellular Organization;
YMR129W	POM152	191a	Intracellular Transport; Cellular Organization;	YJL057C	Cellular Organization; Intracellular Transport; Cellular Organization;
YMR129W	POM152	192a	Intracellular Transport; Cellular Organization;	YMR153W	Cellular Organization; Intracellular Transport; Cellular Organization;
YNL287W	SEC21	193a	Intracellular Transport; Cellular Organization;	YBR281C	Cellular Organization; Intracellular Transport; Cellular Organization;



YDL203C	229a	Metabolism;	YGR058W	229b	Unclassified Proteins;	
YDL203C	230a	Metabolism;	YOR372C	230b	Unclassified Proteins;	
YDR400W	231a	Metabolism;	YCR059C	231b	Unclassified Proteins;	
YHR204W	232a	Metabolism;	YER126C	232b	Unclassified Proteins;	
YLR432W	233a	Metabolism;	YDR459W	233b	Unclassified Proteins;	
YPL059W	234a	Metabolism;	YNL047C	234b	Unclassified Proteins;	
YDL006W	235a	Metabolism; Cell Division And DNA Synthesis; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging; Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;	YDR162C	235b	Protein Destination;	
YDR328C	SKP1	236a	YFL009W	CD4	236b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YGL155W	CDC43	237a	YKL019W	RAM2	237b	Metabolism; Protein Destination; Cellular Organization;
YDR328C	SKP1	238a	YLR352W		238b	Unclassified Proteins;
YPL161C	BEM4	239b	YGL126W	SCS3	239b	Metabolism;
YPL161C	BEM4	240a	YIL163C		240b	Unclassified Proteins;
YPL161C	BEM4	241a	YLR049C		241b	Unclassified Proteins;
YNL236W	SIN4	242a	YJL030W	MAD2	242b	Cell Growth, Cell Division And DNA Synthesis;
YNL236W	SIN4	243a	YGL238W	CSE1	243b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YNL236W	SIN4	244a	YJL013C	MAD3	244b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YNL236W	SIN4	245a	YOR355W	GDS1	245b	Classification Not Yet Clear-Cut;

YDR207C	UME6	246a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOR355W	GDS1	246b	Classification Not Yet Clear-Cut;
YNL236W	SIN4	247a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YFR033C	QCR6	247b	Energy; Cellular Organization;
YNL236W	SIN4	248a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YJR034W	PET191	248b	Energy; Protein Destination; Cellular Organization;
YNL236W	SIN4	249a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YDR054C	CDC34	249b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YNL236W	SIN4	250a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YKL012W	PRP40	250b	Transcription; Cellular Organization;
YNL236W	SIN4	251a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YGR046W		251b	Unclassified Proteins;
YNL236W	SIN4	252a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YGR117C		252b	Unclassified Proteins;
YDR207C	UME6	253a	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YOL082W		253b	Unclassified Proteins;
YGR144W	THI43	254a	Metabolism; Cell Rescue, Defense, Cell Death And Aging;	YGR144W	THI4	254b	Metabolism; Cell Rescue, Defense, Cell Death And Aging;
YER062C	HOR2	255a	Metabolism; Cell Rescue, Defense, Cell Death And Aging;	YPL201C		255b	Unclassified Proteins;
YDR477W	SNF1	256a	Metabolism; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER027C	GAL83	256b	Metabolism; Transcription;
YBR176W	ECM31	257a	Metabolism; Cellular Biogenesis;	YBR176W	ECM31	257b	Metabolism; Cellular Biogenesis;
YDR376W	ARRH1	258a	Metabolism; Cellular Organization;	YIR024C	GIF1	258b	Cell Growth, Cell Division And DNA Synthesis;
YDR408C	ADE8		Metabolism; Cellular Organization;	YGL127C	SOH1		Cell Growth, Cell Division And DNA Synthesis; Transcription;
YDR376W	ARRH1	259a	Metabolism; Cellular Organization;	YCR093W	CDC39	259b	Cell Growth, Cell Division And DNA Synthesis; Transcription;
YDR408C	ADE8	260a	Metabolism; Cellular Organization;	YCR063W		260b	Classification Not Yet Clear-Cut;

YLR438W	CAR2	261a	Metabolism; Cellular Organization; YHL025W	SNF6	261b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YOR180C	EHD2	262a	Metabolism; Cellular Organization; YLR284C	EHD1	262b	Metabolism; Cellular Organization;
YOR202W	HIS3	263a	Metabolism; Cellular Organization; YOR202W	HIS3	263b	Metabolism; Cellular Organization;
YER023W	PRO3	264a	Metabolism; Cellular Organization; YER023W	PRO3	264b	Metabolism; Cellular Organization;
YKL067W	YNK1	265a	Metabolism; Cellular Organization; YKL067W	YNK1	265b	Metabolism; Cellular Organization;
YGL154C	LYS5	266a	Metabolism; Cellular Organization; YGL254W	F2F1	266b	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;
YGR229C	SMI1	267a	Metabolism; Cellular Organization; YKR099W	BA\$1	267b	Metabolism; Transcription; Cellular Organization;
YBL042C	FUJ1	268a	Metabolism; Cellular Organization; YER021W	RPN3	268b	Protein Destination;
YHR128W	FUR1	268a	Metabolism; Cellular Organization; YPR185W	APG13	269b	Protein Destination; Intracellular Transport;
YOR375C	GDH1	270a	Metabolism; Cellular Organization; YJL124C	SPB8	270b	Transcription; Cellular Organization;
YDR408C	ADE8	271a	Metabolism; Cellular Organization; YOR174W	MED4	271b	Transcription; Cellular Organization;
YOR303W	CPA1	272a	Metabolism; Cellular Organization; YOR039W	CKB2	272b	Transcription; Cellular Organization;
YGR061C	ADE6	273a	Metabolism; Cellular Organization; YLR386W	273b	Unclassified Proteins;	
YLR438W	CAR2	274a	Metabolism; Cellular Organization; YGR010W	274b	Unclassified Proteins;	
YLR438W	CAR2	275a	Metabolism; Cellular Organization; YLR328W	275b	Unclassified Proteins;	
YOL059W	GPD2	276a	Metabolism; Cellular Organization; YFL017C	276b	Unclassified Proteins;	
YNL104C	LEU4	277a	Metabolism; Cellular Organization; YKL183W	277b	Unclassified Proteins;	
YLR345W		278a	Metabolism; Energy; YLR321C	SFH1	278b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Biogenesis; Cellular Organization;
-	-	-	-	-	-	-
YJL137C	GLG2	279a	Metabolism; Energy; YJL137C	GLG2	279b	Metabolism; Energy;
YGL134W	PCL10	280a	Metabolism; Energy; YPL031C	PHO85	280b	Metabolism; Energy; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YLR345W		281a	Metabolism; Energy; YGR158C	MTR3	281b	Transcription; Cellular Organization;
YKR096W		282a	Metabolism; Energy; Cell Growth, YBL051C		282b	Unclassified Proteins;
YER133W	GLC7	283a	Metabolism; Energy; Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization; BN14		283b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;

YLR071C	RGR1	284a	Metabolism; Energy; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;	YDL065C	PEX19	284b	Cellular Organization;
YDR074W	TPS2	285a	Metabolism; Energy; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER019C-A	SBH2	285b	Protein Destination; Transport Facilitation; Intracellular Transport; Unclassified Proteins;
YDR074W	TPS2	286a	Metabolism; Energy; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YAR066W		286b	
YBR221C	PDB1	287a	Metabolism; Energy; Cellular Organization;	YLR345W		287b	Metabolism; Energy; Protein Destination;
YDR148C	KGD2	288a	Metabolism; Energy; Cellular Organization;	YDR510W	SMT3	288b	Protein Synthesis; Cellular Organization; Unclassified Proteins;
YMR267W	PPA2	289a	Metabolism; Energy; Cellular Organization;	YKR026C	GCN3	289b	DNA Synthesis; Cellular Organization;
YDR001C		290a	Metabolism; Energy; Cellular Organization;	YLR270W		290b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;
YCL040W	GLK1	291a	Metabolism; Energy; Intracellular Transport; Cellular Organization;	YBR040W	FIG1	291b	Metabolism; Transcription; Cellular Organization;
YCL040W	GLK1	292a	Metabolism; Energy; Intracellular Transport; Cellular Organization;	YML099C	ARG81	292b	Cellular Organization;
YMR079W	SEC14	293a	Metabolism; Intracellular Transport; Cellular Organization;	YDL001W		293b	Unclassified Proteins;
YDL090C	RAM1	294a	Metabolism; Protein Destination; Signal Transduction; Cellular Organization;	YKL019W	RAM2	294b	Metabolism; Protein Destination; Cellular Organization;
YLR150W	STM1	295a	Metabolism; Signal Transduction; YJR072C			295b	Unclassified Proteins;
YGL254W	FZF1	298a	Metabolism; Transcription; Cell Rescue, Cell Death And Aging; Cellular Organization;	YHR215W	PHO12	296b	Metabolism; Cellular Organization;
YGL115W	SNF4	297a	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YER027C	GAL83	297b	Metabolism; Transcription;
YGL254W	FZF1	298a	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YOR039W	CKB2	298b	Transcription; Cellular Organization;
YGL254W	FZF1	299a	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YGR047C	TFC4	299b	Transcription; Cellular Organization;
YOL108C	INO4	300a	Metabolism; Transcription; Cellular Organization;	YKL017C	HCS1	300b	Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis;
YOL108C	INO4	301a	Metabolism; Transcription; Cellular Organization;	YMR317W		301b	
YNL314W	DAL82	302a	Metabolism; Transcription; Cellular Organization;	YNL314W	DAL82	302b	Metabolism; Transcription; Cellular Organization; Metabolism; Transcription;
YOL108C	INO4	303a	Metabolism; Transcription;	YDR123C	INO2	303b	

YOL108C	INO4	304a	Cellular Organization; Metabolism; Transcription; Cellular Organization;	YKL135C	APL2	304b	Cellular Organization; Protein Destination; Intracellular Transport; Cellular Organization;
YJL110C	GZF3	305a	Metabolism; Transcription; Cellular Organization;	YNL021W	HDA1	305b	Transcription; Protein Destination; Cellular Organization;
YOL108C	INO4	306a	Metabolism; Transcription; Cellular Organization; Metabolism; Transport Facilitation; Intracellular Transport; Cellular Organization;	YNL279W		306b	Unclassified Proteins;
YOR348C	PUT4	307a	Metabolism; Transport Facilitation; YMR229W	MTF1		307b	Cell Growth; Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YOR348C	PUT4	308a	Metabolism; Transport Facilitation; YCR045C			308b	Protein Destination;
YOR348C	PUT4	309a	Metabolism; Transport Facilitation; YJL084C			309b	Unclassified Proteins;
YOR348C	PUT4	310a	Intracellular Transport; Cellular Organization; Metabolism; Transport Facilitation; YLR294C			310b	Unclassified Proteins;
YMR091C	NPL6	311a	Intracellular Transport; Cellular Organization; Protein Destination;	YFR037C	RSC8	311b	Cell Growth; Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YER144C	UBP5	312a	Protein Destination;	YBR059C		312b	Classification Not Yet Clear-Cut;
YLR417W	VPS36	313a	Protein Destination;	YPL002C	SNF8	313b	Metabolism; Transcription;
YDL097C	RPN6	314a	Protein Destination;	YEI009C	GCN4	314b	Cellular Organization;
YDR394W	RPT3	315a	Protein Destination;	YGR232W		315b	Protein Destination;
YPL003W	U1A1	316a	Protein Destination;	YPR066W	UBA3	316b	Protein Destination;
YOR132W	VPS17	317a	Protein Destination;	YOR069W	VPS5	317b	Protein Destination; Cellular Organization;
YDR098C		318a	Protein Destination;	YGL071W	RCS1	318b	Transcription; Ionic Homeostasis;
YER174C		319a	Protein Destination;	YGL071W	RCS1	319b	Cellular Organization;
YML094W	GLM5	320a	Protein Destination;	YLR200W	YKE2	320b	Transcription; Ionic Homeostasis;
YOL111C		321a	Protein Destination;	YOR007C	SGT2	321b	Unclassified Proteins;
YHR057C	CYP2	322a	Protein Destination; Cell Rescue, Defense, Cell Death And Aging;	YJR091C	JSN1	322b	Unclassified Proteins;
YPL149W	APG5	323a	Cellular Organization; Protein Destination; Cellular Biogenesis; Cellular Organization;	YBR217W		323b	Cell Growth; Cell Division And DNA Synthesis;
YPL149W	APG5	324a	Protein Destination; Cellular Biogenesis; Cellular Organization;	YMR159C	SAP18	324b	Protein Destination; Cellular Biogenesis; Cellular Organization;
YBR217W		325a	Protein Destination; Cellular Biogenesis; Cellular Organization;	YMR159C	SAP18	325b	Unclassified Proteins;

YMR314W	PRE5	326a	Protein Destination; Cellular Organization;	YKL130C	SHE2	326b	Cell Growth, Cell Division And DNA Synthesis; Cellular Organization;	
YPR051W	MAK3	327a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YEL053C	MAK10	327b	Energy;	
YNL135C	FPR1	328a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YER052C	HOM3	328b	Metabolism;	
YKL103C	LAP4	329a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YKL103C	LAP4	329b	Protein Destination; Cellular Organization; Protein Destination; Transport Facilitation; Intracellular Transport; Ionic Homeostasis;	
YHR060W	VMA22	330a	Protein Destination; Cellular Organization;	YLR447C	VMA6	330b	Cellular Organization; Cellular Organization; Protein Synthesis; Cellular Organization; Unclassified Proteins;	
YOL088C	MPD2	331a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YHR091C	MSR1	331a	Unclassified Proteins;	
YKL103C	LAP4	332a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YOL082W		332b	Unclassified Proteins;	
YOL088C	MPD2	333a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YLR312C		333b	Unclassified Proteins;	
YEL060C	PRB1	334a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YML032C-A		334b	Unclassified Proteins;	
-	YOR362C	PRE10	335a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YFL017C	335b	Unclassified Proteins;	
-	YDR292C	SRP101	336a	Protein Destination; Cellular Organization; Protein Destination; Cellular Organization;	YMR163C	336b	Unclassified Proteins;	
-	YHR060W	VMA22	337a	Protein Destination; Cellular Organization; Protein Destination; Intracellular Transport;	YDR469W	337b	Unclassified Proteins;	
-	YPR185W	APG13	338a	Protein Destination; Intracellular Transport;	YGL180W	APG1	338b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Intracellular Transport; Cellular Organization; Cell Growth Cell Division And DNA Synthesis; Protein Destination; Cell Rescue, Defense, Cell Death And Aging;
-	YPR185W	APG13	339a	Protein Destination; Intracellular Transport;	YGR253C	PUP2	339b	Cellular Organization; Intracellular Transport; Cellular Organization; Protein Destination;
-	YBR170C	NPL4	340a	Protein Destination; Intracellular Transport; Protein Destination; Intracellular Transport;	YGR120C		340b	Cellular Organization; Intracellular Transport; Cellular Organization;
-	YPR185W	APG13	341a	Protein Destination; Intracellular Transport; Protein Destination; Intracellular Transport;	YGR048W	UFD1	341b	Protein Destination;
-	YNL093W	YPT53	342a	Protein Destination; Intracellular Transport;	YNL086W		342b	Unclassified Proteins;
-	YPR173C	VPS4	343a	Protein Destination; Intracellular Transport;	YNL032W	SIW14	343b	Unclassified Proteins;
-	YPR173C	VPS4	344a	Protein Destination; Intracellular Transport; Cellular Biogenesis; Cellular Organization;	YLR025W	SNF7	344b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;

YPL259C	APM1	345a	YKL135C	APL2	345b	Protein Destination; Intracellular Transport; Cellular Biogenesis; Cellular Organization;	Protein Destination; Intracellular Transport; Cellular Organization;	345b
YJL154C	VPS35	346a	YGL166W	CUP2	346b	Transcription; Ionic Homeostasis; Cellular Organization;	Transcription; Ionic Homeostasis; Cellular Organization;	346b
YDR142C	PEX7	347a	YIL160C	POT1	347b	Metabolism; Energy; Cellular Organization; Signal Transduction;	Metabolism; Energy; Cellular Organization; Signal Transduction;	347b
YNR006W	VPS27	348a	YHL002W		348b	Unclassified Proteins;	Unclassified Proteins;	348b
YDR142C	PEX7	349a	YGR239C		349b	Unclassified Proteins;	Unclassified Proteins;	349b
YDR142C	PEX7	350a	YHR160C		350b	Unclassified Proteins;	Unclassified Proteins;	350b
YDL212W	SHR3	351a	YDR508C	GNP1	351b	Metabolism; Transport Facilitation;	Metabolism; Transport Facilitation;	351b
YDR115W		352a	YKL142W	MRP8	352b	Protein Synthesis; Cellular Organization;	Protein Synthesis; Cellular Organization;	352b
YER102W	RPS8B	353a	YBR135W	CKS1	353b	Cell Growth; Cell Division And DNA Synthesis;	Cell Growth; Cell Division And DNA Synthesis;	353b
YOR276W	CAF20	354a	YOL139C	CDC33	354b	Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization; Energy; Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis;	Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization; Energy; Cell Growth, Cell Division And DNA Synthesis; Cellular Biogenesis;	354b
YKL142W	MRP8	355a	YMR165C	SMP2	355b	Protein Synthesis; Cellular Organization;	Protein Synthesis; Cellular Organization;	355b
YKR026C	GCN3	356a	YKR026C	GCN3	356b	Protein Synthesis; Cellular Organization;	Protein Synthesis; Cellular Organization;	356b
YKL142W	MRP8	357a	YKL142W	MRP8	357b	Protein Synthesis; Cellular Organization;	Protein Synthesis; Cellular Organization;	357b
YMR309C	NIP1	358a	YNL244C	SUJ1	358b	Protein Synthesis; Cellular Organization;	Protein Synthesis; Cellular Organization;	358b
YLR264W	RPS28B	359a	YOL149W	DCP1	359b	Protein Synthesis; Cellular Organization;	Protein Synthesis; Cellular Organization;	359b
YLR291C	GCD7	360a	YPL070W		360b	Unclassified Proteins;	Unclassified Proteins;	360b
YMR309C	NIP1	361a	YNL047C		361b	Unclassified Proteins;	Unclassified Proteins;	361b
YMR309C	NIP1	362a	YOF284W		362b	Unclassified Proteins;	Unclassified Proteins;	362b
YGL189C	RPS26A	363a	YLR435W		363b	Unclassified Proteins;	Unclassified Proteins;	363b
YER311W	RPS26B	364a	YLR435W		364b	Unclassified Proteins;	Unclassified Proteins;	364b
YLP264W	RPS28B	365a	YBR094W		365b	Unclassified Proteins;	Unclassified Proteins;	365b
YER012W	RPS8B	366a	YFL017C		366b	Unclassified Proteins;	Unclassified Proteins;	366b

YDR429C	TIF35	367a	Organization; Protein Synthesis; Cellular Organization; Retrotransposons And Plasmid Proteins;	YFL017C	367b	Unclassified Proteins;
YCR020C- A	MAK31	368a	Signal Transduction; Signal Transduction;	YEL053C	368b	Energy;
YHR158C	KEL1	369a	Signal Transduction;	YOR047C	369b	Metabolism; Transcription;
YHR158C	KEL1	370a	Signal Transduction;	YJR122W	370b	Transcription; Cellular Organization;
YHR158C	KEL1	371a	Signal Transduction;	YMR181C	371b	Unclassified Proteins;
YCR027C		372a	Signal Transduction;	YOL083W	372b	Unclassified Proteins;
YHL002W		373a	Signal Transduction;	YNR005C	373b	Unclassified Proteins;
YKL166C	TPK3	374a	Signal Transduction; Cellular Organization;	YIL033C	374b	Metabolism; Cell Growth; Cell Division And DNA Synthesis; Cell Rescue; Defense; Cell Death And Aging; Cellular Organization;
YDR017C	KCS1	375a	Transcription;	YDR099W	375b	Cell Growth; Cell Division And DNA Synthesis;
YOR025W	HST3	376a	Transcription;	YLR403W	376b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
-	YIL105C	377a	Transcription;	YER179W	377b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
-	YDR026C	378a	Transcription;	YDR110W	378b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
-	YIL105C	379a	Transcription;	YKL130C	379b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
YML015C	TAF40	380a	Transcription;	YDR174W	380b	Cellular Organization;
YGL150C	INO80	381a	Transcription;	YOR355W	381b	Classification Not Yet Clear-Cut;
YGL150C	INO80	382a	Transcription;	YDL002C	382b	Classification Not Yet Clear-Cut;
YER127W	LCP5	383a	Transcription;	YDR299W	383b	Intracellular Transport;
YPR107C	YTH1	384a	Transcription;	YBR205W	384b	Metabolism; Protein Destination;
YGL221C	NIF3	385a	Transcription;	YGL221C	385b	Transcription;
YML015C	TAF40	386a	Transcription;	YDR167W	386b	Transcription; Cellular Organization;
YPR107C	YTH1	387a	Transcription;	YJR093C	387b	Transcription; Cellular Organization;
YDR439W	LRS4	388a	Transcription;	YCR086W	388b	Unclassified Proteins;
YCR004C	YCP4	389a	Transcription;	YDR032C	389b	Unclassified Proteins;
YER116C		390a	Transcription;	YGR024C	390b	Unclassified Proteins;
YIL105C		391a	Transcription;	YNL047C	391b	Unclassified Proteins;
YR005W		392a	Transcription;	YGL174W	392b	Unclassified Proteins;
YDR311W	TFB1	393a	Transcription; Cell Rescue, Defense; Cell Death And Aging; Cellular Organization;	YGR120C		Intracellular Transport; Cellular Organization;

YDR311W	TFB1	394a	Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YKL103C	LAP4	394b	Protein Destabilization; Cellular Organization;	
YDR311W	TFB1	395a	Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	YOL082W		395b	Unclassified Proteins;	
YDR225W	HTA1	396a	Transcription; Cellular Organization;	YKR048C	NAP1	396b	Cell Growth, Cell Division And DNA Synthesis; Protein Destabilization; Cellular Biogenesis; Cellular Organization; Metabolism; Cell Growth, Cell Division And DNA Synthesis;	
YMR112C		397a	Transcription; Cellular Organization;	YBR253W	SRB6	397b	Transcription; Cellular Organization; Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization; Protein Synthesis; Cellular Organization; Transcription;	
YGL208W	SIP2	398a	Transcription; Cellular Organization;	YGL115W	SNF4	398b	Transcription; Cellular Organization; Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization; Protein Synthesis; Cellular Organization; Transcription;	
YGL122C	NAB2	399a	Transcription; Cellular Organization;	YKR026C	GCN3	399b	Transcription; Cellular Organization; Transcription;	
YDL160C	DHH1	400a	Transcription; Cellular Organization;	YOL149W	DCP1	400b	Transcription;	
-	YGR158C	MTR3	401a	Transcription; Cellular Organization;	YDL111C	RRP42	401b	Transcription;
YKL028W	TFA1	402a	Transcription; Cellular Organization;	YDR311W	TFB1	402b	Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	
YGL237C	HAP2	403a	Transcription; Cellular Organization;	YBL021C	HAP3	403b	Transcription; Cellular Organization;	
YGL237C	HAP2	404a	Transcription; Cellular Organization;	YOR358W	HAP5	404b	Transcription; Cellular Organization;	
YBL021C	HAP3	405a	Transcription; Cellular Organization;	YGL122C	NAB2	405b	Transcription; Cellular Organization;	
YOL123W	HRP1	406a	Transcription; Cellular Organization;	YOR174W	MED4	406b	Transcription; Cellular Organization;	
YOL135G	MED7	407a	Transcription; Cellular Organization;	YBL014C	RRN6	407b	Transcription; Cellular Organization;	
YPR110C	RPC40	408a	Transcription; Cellular Organization;	YNL113W	RPC19	408b	Transcription; Cellular Organization;	
YJL025W	RRN7	409a	Transcription; Cellular Organization;	YBL025W	RRN10	409b	Transcription; Cellular Organization;	
YMR270C	RRN9	410a	Transcription; Cellular Organization;	YPR182W	SMX3	410b	Transcription; Cellular Organization;	
YOR159C	SME1	411a	Transcription; Cellular Organization;	YLR275W	SMD2	411b	Transcription; Cellular Organization;	
YPR182W	SMX3	412a	Transcription; Cellular Organization;	YBR193C	MED8	412b	Transcription; Cellular Organization;	
YGR104C	SRB5	413a	Transcription; Cellular Organization;			413b	Transcription; Cellular Organization;	

YDR308C	SRB7	414a	Transcription; Cellular Organization;	YOR174W	MED4	414b	Transcription; Cellular Organization;
YDR308C	SRB7	415a	Transcription; Cellular Organization;	YOL135C	MED7	415b	Transcription; Cellular Organization;
YGL112C	TAF60	416a	Transcription; Cellular Organization;	YMR236W	TAF17	416b	Transcription; Cellular Organization;
YKL028W	TFA1	417a	Transcription; Cellular Organization;	YKR062W	TFA2	417b	Transcription; Cellular Organization;
YOR210W	RPB10	418a	Transcription; Cellular Organization;	YGL166W	CUP2	418b	Transcription; Ionic Homeostasis;
YIR018W	YAP5	419a	Transcription; Cellular Organization;	YGL071W	RCS1	419b	Cellular Organization;
YDL160C	DHH1	420a	Transcription; Cellular Organization;	YEL015W		420b	Transcription; Ionic Homeostasis;
YPR110C	RPC40	421a	Transcription; Cellular Organization;	YLR238W		421b	Unclassified Proteins;
YDL150W	RPC53	422a	Transcription; Cellular Organization;	YKR025W		422b	Unclassified Proteins;
YDR088C	SLU7	423a	Transcription; Cellular Organization;	YDL144C		423b	Unclassified Proteins;
YMR039C	SUB1	424a	Transcription; Cellular Organization;	YMR316C-B		424b	Unclassified Proteins;
- YGL112C	TAF60	425a	Transcription; Cellular Organization;	YMR255W		425b	Unclassified Proteins;
YDR002W		426a	Transcription; Intracellular Transport; Cellular Organization;	YKR048C	NAP1	426b	Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis;
YLR293C	GSP1	427a	Transcription; Intracellular Transport; Cellular Organization;	YJR074W	MOG1	427b	Cellular Organization;
YOR185C	GSP2	428a	Transcription; Intracellular Transport; Cellular Organization;	YJR074W	MOG1	428b	Unclassified Proteins;
YLR216C	CPR6	429a	Transcription; Protein Destination; Cellular Organization;	YIR037W	HYR1	429b	Cell Rescue, Defense, Cell Death And Aging;
YBR237W	PRP5	430a	Transcription; Protein Destination; Cellular Organization;	YDR073W	SNF11	430b	Metabolism; Cell Growth, Cell Division And DNA Synthesis;
YGR252W	GCN5	431a	Transcription; Protein Destination; Cellular Organization;	YDR448W	ADA2	431b	Transcription; Cellular Organization;
YBR052C		432a	Transport Facilitation;	YDR032C		432b	Transport Facilitation; Cellular Organization;
YKR104W		433a	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;	YOL143C	RIB4	433b	Unclassified Proteins; Metabolism;
YLL028W		434a	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;	YGL166W	CUP2	434b	Transcription; Ionic Homeostasis;
YIL013C	PDR11	435a	Transport Facilitation; Cellular Organization;	YDR174W		435b	Cellular Organization;

YOL130W	ALR1	436a	Organization; Transport; Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization; Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization; Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YGL025C	PGD1	436b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YOL130W	ALR1	437a	Organization; Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YLR291C	GCD7	437b	Protein Synthesis; Cellular Organization;
YMR243C	ZRC1	438a	Organization; Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YKL142W	MRP8	438b	Protein Synthesis; Cellular Organization;
YOL130W	ALR1	439a	Organization; Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YGL024W		439b	Unclassified Proteins;
YOL130W	ALR1	440a	Organization; Transport Facilitation; Intracellular Transport; Cell Rescue, Defense, Cell Death And Aging; Ionic Homeostasis; Cellular Organization;	YNL086W		440b	Unclassified Proteins;
YFL060C	SNO3	441a	Unclassified Proteins;	YMR096W	SNZ1	441b	Cell Growth, Cell Division And DNA Synthesis;
YDL012C		442a	Unclassified Proteins;	YDR151C	CTH1	442b	Cell Growth, Cell Division And DNA Synthesis;
YIL065C		443a	Unclassified Proteins;	YJR091C	JSN1	443b	Cell Growth, Cell Division And DNA Synthesis;
YLR392C		444a	Unclassified Proteins;	YJR091C	JSN1	444b	Cell Growth, Cell Division And DNA Synthesis;
YDR214W		445a	Unclassified Proteins;	YJL030W	MAD2	445b	Cell Growth, Cell Division And DNA Synthesis;
YNL127W		446a	Unclassified Proteins;	YKR055W	RHO4	446b	Cell Growth, Cell Division And DNA Synthesis;
YGR278W		447a	Unclassified Proteins;	YGR049W	SCM4	447b	Cell Growth, Cell Division And DNA Synthesis;
YMR322C		448a	Unclassified Proteins;	YMR096W	SNZ1	448b	Cell Growth, Cell Division And DNA Synthesis;
YBR190W		449a	Unclassified Proteins;	YLR117C	SYF3	449b	Cell Growth, Cell Division And DNA Synthesis;
YDL012C		450a	Unclassified Proteins;	YJL065C		450b	Cell Growth, Cell Division And DNA Synthesis;
YNR029C		451a	Unclassified Proteins;	YJL065C		451b	Cell Growth, Cell Division And DNA Synthesis;

YGL061C	DUO1	452a	Unclassified Proteins;	YER016W	BIM1	452b	Cell Growth; Cell Division And DNA Synthesis; Cellular Biogenesis; Cellular Organization;
YOR353C		453a	Unclassified Proteins;	YHR102W	NRK1	453b	Cell Growth; Cell Division And DNA Synthesis; Cellular Biogenesis;
YBR141C		454a	Unclassified Proteins;	YGL091C	NBP35	454b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
YGR154C		455a	Unclassified Proteins;	YCR057C	PWP2	455b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
YGR017W		456a	Unclassified Proteins;	YLR403W	SFP1	456b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
YJL048C		457a	Unclassified Proteins;	YKL130C	SHE2	457b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
YPR020W		458a	Unclassified Proteins;	YKL130C	SHE2	458b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
-	YDL239C	459a	Unclassified Proteins;	YHR184W	SSP1	459b	Cell Growth; Cell Division And DNA Synthesis; Cellular Organization;
-	YNL078W	460a	Unclassified Proteins;	YKR048C	NAP1	460b	Cell Growth; Cell Division And DNA Synthesis; Protein Destination; Cellular Biogenesis; Cellular Organization;
YDR315C		461a	Unclassified Proteins;	YJR117W	STE24	461b	Cell Growth; Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YLR200W	YKE2	462a	Unclassified Proteins;	YMR052W	FAR3	462b	Cell Growth; Cell Division And DNA Synthesis; Signal Transduction;
YDR200C		463a	Unclassified Proteins;	YMR052W	FAR3	463b	Cell Growth; Cell Division And DNA Synthesis; Signal Transduction;
YDR032C		464a	Unclassified Proteins;	YCL032W	STE50	464b	Cell Growth; Cell Division And DNA Synthesis; Signal Transduction;
YNL127W		465a	Unclassified Proteins;	YAL016W	TPD3	465b	Cell Growth; Cell Division And DNA Synthesis; Transcription;
YIL065C		466a	Unclassified Proteins;	YLR321C	SFH1	466b	Cell Growth; Cell Division And DNA Synthesis; Transcription; Cellular Biogenesis; Cellular Organization;

YIL132C	467a	Unclassified Proteins;	YLR321C	SFH1	467b	Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Biogenesis; Cellular Organization;
YGL230C	468a	Unclassified Proteins;	YKL110C	KT112	468b	Cell Rescue, Defense, Cell Death And Aging;
YBL101W-	469a	Unclassified Proteins;	YBL043W	ECM13	469b	Cellular Biogenesis;
A						
YGR068C	470a	Unclassified Proteins;	YBL102W	SFT2	470b	Cellular Organization;
YKL090W	471a	Unclassified Proteins;	YPL128C	TBF1	471b	Cellular Organization;
YPL260W	472a	Unclassified Proteins;	YIL144W	TID3	472b	Cellular Organization;
YKL002W	473a	Unclassified Proteins;	YMR117C		473b	Cellular Organization;
YBR141C	474a	Unclassified Proteins;	YDR372C		474b	Cellular Organization;
						Unclassified Proteins;
YMR095C	SNO1	475a	Unclassified Proteins;	YNL333W	SNZ22	Classification Not Yet Clear-Cut;
YFL060C	SNO3	476a	Unclassified Proteins;	YNL333W	SNZ22	Classification Not Yet Clear-Cut;
YDL012C		477a	Unclassified Proteins;	YOR355W	GDS1	Classification Not Yet Clear-Cut;
YNL091W		478a	Unclassified Proteins;	YOR355W	GDS1	Classification Not Yet Clear-Cut;
YMR312W		479a	Unclassified Proteins;	YHR187W	IK1	Classification Not Yet Clear-Cut;
YMR322C		480a	Unclassified Proteins;	YNL333W	SNZ22	Classification Not Yet Clear-Cut;
YMR322C		481a	Unclassified Proteins;	YFL059W	SNZ23	Classification Not Yet Clear-Cut;
YDR071C		482a	Unclassified Proteins;	YBR125C	481b	Classification Not Yet Clear-Cut;
YDR82C		483a	Unclassified Proteins;	YGL028C	482b	Classification Not Yet Clear-Cut;
YMR102C		484a	Unclassified Proteins;	YNL218W	483b	Classification Not Yet Clear-Cut;
YJL112W		485a	Unclassified Proteins;	YLL001W	DNM1	Intracellular Transport; Cellular Biogenesis;
						Intracellular Transport; Cellular Organization;
YDR472W	486a	Unclassified Proteins;	YKR068C	BET3	486b	Intracellular Transport; Cellular Organization;
YDR128W	487a	Unclassified Proteins;	YLR208W	SEC13	487b	Intracellular Transport; Cellular Organization;
YPR105C	488a	Unclassified Proteins;	YGL145W	TIP20	488b	Intracellular Transport; Cellular Organization;
YAL034W-	489a	Unclassified Proteins;	YGR120C		489b	Intracellular Transport; Cellular Organization;
A			YBR254C		490b	Intracellular Transport; Cellular Organization;
YDR472W	490a	Unclassified Proteins;	YGR120C		491b	Intracellular Transport; Cellular Organization;
YER157W	491a	Unclassified Proteins;	YGR120C		492b	Intracellular Transport; Cellular Organization;
YNR025C	492a	Unclassified Proteins;	YGR120C		493b	Intracellular Transport; Cellular Organization;
YPR105C	493a	Unclassified Proteins;	YGR120C		494b	Intracellular Transport; Cellular Organization;
YFL010C	495a	Unclassified Proteins;	YDR515W	SLF1	495b	Ionic Homeostasis;
YELO41W	496a	Unclassified Proteins;	YJR049C	UTR1	496b	Ionic Homeostasis;
YGR163W	497a	Unclassified Proteins;	YML121W	GTR1	497b	Metabolism;
YNL311C	498a	Unclassified Proteins;	YKL001C	MET14	498b	Metabolism;

YOR138C YLL062C YBL101W- A	499a 500a 501a	Unclassified Proteins; Unclassified Proteins; Unclassified Proteins;	YEL062W YOL143C YNL229C	NPR2 RIB4 URE2	499b 500b 501b	Metabolism; Metabolism; Metabolism;
YDL012C YDR132C YGR294W YIL008W YNL311C YFR042W	502a 503a 504a 505a 506a 507a	Unclassified Proteins; Unclassified Proteins; Unclassified Proteins; Unclassified Proteins; Unclassified Proteins; Unclassified Proteins;	YFR047C YJL218W YHL018W YHR111W YIL074C YPR159W	502b 503b 504b 505b 506b 507b	Metabolism; Metabolism; Metabolism; Metabolism; Metabolism; Metabolism;	Metabolism; Metabolism; Metabolism; Metabolism; Metabolism; Metabolism;
YML088W	508a	Unclassified Proteins;	YDR328C	SKP1	508b	Cell Division And DNA Synthesis; Cellular Biogenesis; Cellular Organization;
YGR122W	509a	Unclassified Proteins;	YLR025W	SNF7	509b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
YMR025W	510a	Unclassified Proteins;	YNR052C	POP2	510b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Protein Destination; Cellular Organization;
-	YML068W	511a	Unclassified Proteins;	YDR073W	SNF11	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YNL034W	512a	Unclassified Proteins;	YNL025C	SSN8	512b	Metabolism; Cell Growth, Cell Division And DNA Synthesis; Transcription; Cellular Organization;
YDR215C	513a	Unclassified Proteins;	YPL175W	SPT14	513b	Metabolism; Cellular Biogenesis; Cellular Organization;
YAL032C YLR465C YDL012C YAR014C	514a 515a 516a 517a	Unclassified Proteins; Unclassified Proteins; Unclassified Proteins; Unclassified Proteins;	YLR345W YML035C YIL172C YER133W	AMD1 GLC7	514b 515b 516b 517b	Metabolism; Energy; Metabolism; Energy; Metabolism; Energy; Cell Growth, Cell Division And DNA Synthesis; Protein Synthesis; Cellular Organization;
YML053C	518a	Unclassified Proteins;	YJR009C	TDH2	518b	Metabolism; Energy; Cellular Organization;
YGR058W	519a	Unclassified Proteins;	YLR113W	HOG1	519b	Metabolism; Signal Transduction; Cell Rescue, Defense, Cell Death And Aging;

YCL046W	520a	Unclassified Proteins;	YGL115W	SNF4	520b	Metabolism; Transcription; Cell Rescue, Defense, Cell Death And Aging; Cellular Organization;	
YPL039W	MET31	521a	Unclassified Proteins;	YEL009C	GCN4	521b	Metabolism; Transcription; Cellular Organization;
YGL242C		522a	Unclassified Proteins;	YKR099W	BAS1	522b	Metabolism; Transcription; Cellular Organization;
YDL076C		523a	Unclassified Proteins;	YLR098C	CHA4	523b	Metabolism; Transcription; Cellular Organization;
YDL239C		524a	Unclassified Proteins;	YLR098C	CHA4	524b	Metabolism; Transcription; Cellular Organization;
YHR145C		525a	Unclassified Proteins;	YEL009C	GCN4	525b	Metabolism; Transcription; Cellular Organization;
YDL110C		526a	Unclassified Proteins;	YKL015W	PUT3	526b	Metabolism; Transcription; Cellular Organization;
YGL230C		527a	Unclassified Proteins;	YDL210W	UGA4	527b	Metabolism; Transport Facilitation; Intracellular Transport; Cellular Organization;
YPL222W		528a	Unclassified Proteins;	YGR048W	UFD1	528b	Protein Destinination;
YIL151C		529a	Unclassified Proteins;	YLR121C	YPS4	529b	Protein Destinination;
YLL049W		530a	Unclassified Proteins;	YNR069C		530b	Protein Destinination;
YNR068C		531a	Unclassified Proteins;	YNR069C		531b	Protein Destinination;
YAR031W		532a	Unclassified Proteins;	YBR217W		532b	Protein Destinination; Cellular Biogenesis; Cellular Organization;
YAL034W-A		533a	Unclassified Proteins;	YKL103C	LAP4	533b	Protein Destinination; Cellular Organization;
YPL019C		534a	Unclassified Proteins;	YHR060W	VMA22	534b	Protein Destinination; Cellular Organization;
YPR105C		535a	Unclassified Proteins;	YHR060W	VMA22	535b	Protein Destinination; Cellular Organization;
YOL105C	WSC3	536a	Unclassified Proteins;	YGL153W	PEX14	536b	Protein Destinination; Intracellular Transport; Cellular Organization;
YBR077C		537a	Unclassified Proteins;	YMR004W	MVP1	537b	Protein Destinination; Intracellular Transport; Cellular Organization;
YPL151C		538a	Unclassified Proteins;	YOR036W	PEP12	538b	Protein Destinination; Intracellular Transport; Cellular Organization;
YPR105C		539a	Unclassified Proteins;	YGL153W	PEX14	539b	Protein Destinination; Intracellular Transport; Cellular Organization;
YDR482C		540a	Unclassified Proteins;	YOR276W	CAF20	540b	Protein Synthesis; Cellular Organization;
YBR270C		541a	Unclassified Proteins;	YKR026C	GCN3	541b	Protein Synthesis; Cellular Organization;
YER186C		542a	Unclassified Proteins;	YKR026C	GCN3	542b	Protein Synthesis; Cellular Organization;
YMR269W		543a	Unclassified Proteins;	YKR026C	GCN3	543b	Protein Synthesis; Cellular Organization;
YER082C		544a	Unclassified Proteins;	YKL142W	MRP8	544b	Protein Synthesis; Cellular Organization;

YMR210W	<b>545a</b>	Unclassified Proteins;	YKL142W	MRP8	<b>545b</b>
YDL063C	<b>546a</b>	Unclassified Proteins;	YPL131W	RPL5	<b>546b</b>
YLL027W	<b>547a</b>	Unclassified Proteins;	YGL189C	RPS26A	<b>547b</b>
YLL027N	<b>548a</b>	Unclassified Proteins;	YER131W	RPS26B	<b>548b</b>
YDR315C	<b>549a</b>	Unclassified Proteins;	YLR264W	RPS28B	<b>549b</b>
YCL020W	<b>550a</b>	Unclassified Proteins;	YFL002W-A		<b>550b</b>
YFL010C	<b>551a</b>	Unclassified Proteins;	YGR136W		<b>551b</b>
YGR058W	<b>552a</b>	Unclassified Proteins;	YGR136W		<b>552b</b>
YDR416W	<b>553a</b>	Unclassified Proteins;	YBR188C	NTC20	<b>553b</b>
YDR215C	<b>554a</b>	Unclassified Proteins;	YKR024C	DBP7	<b>554b</b>
YDR132C	<b>555a</b>	Unclassified Proteins;	YHR170W	NMD3	<b>555b</b>
YBR270C	<b>556a</b>	Unclassified Proteins;	YIL105C		<b>556b</b>
YDL146W	<b>557a</b>	Unclassified Proteins;	YKL070W		<b>557b</b>
YDR326C	<b>558a</b>	Unclassified Proteins;	YIL105C		<b>558b</b>
YGR250C	<b>559a</b>	Unclassified Proteins;	YIR001C		<b>559b</b>
YMR068W	<b>560a</b>	Unclassified Proteins;	YIL105C		<b>560b</b>
YPR082C	<b>561a</b>	Unclassified Proteins;	YBR055C	PRP6	<b>561b</b>
YDR313C	<b>562a</b>	Unclassified Proteins;	YPL133C	YPL133C	<b>562b</b>
YGR068C	<b>563a</b>	Unclassified Proteins;	YGL019W	CKB1	<b>563b</b>
YMR255W	<b>564a</b>	Unclassified Proteins;	YGL122C	NAB2	<b>564b</b>
YDL098C	<b>565a</b>	Unclassified Proteins;	YGR075C	PRP38	<b>565b</b>
YFL023W	<b>566a</b>	Unclassified Proteins;	YBR154C	RPB5	<b>566b</b>
YDR255C	<b>567a</b>	Unclassified Proteins;	YKL144C	RPC25	<b>567b</b>
YDR357C	<b>568a</b>	Unclassified Proteins;	YPR182W	SMX3	<b>568b</b>
YOL106W	<b>569a</b>	Unclassified Proteins;	YPR182W	SMX3	<b>569b</b>
YBR270C	<b>570a</b>	Unclassified Proteins;	YMR236W	TAF17	<b>570b</b>
YML114C	<b>571a</b>	Unclassified Proteins;	YDR167W	TAF25	<b>571b</b>
YDL063C	<b>572a</b>	Unclassified Proteins;	YDR381W	YRA1	<b>572b</b>

YNL171C	573a	Unclassified Proteins;	YCR106W	573b	Organization; Transcription; Cellular Organization;
YAL034W- A	574a	Unclassified Proteins;	YGL172W	574b	Transcription; Intracellular Transport; Cellular Organization;
YKR011C	575a	Unclassified Proteins;	YGL166W	575b	Transcription; Ionic Homeostasis; Cellular Organization;
YML006C	576a	Unclassified Proteins;	YGL166W	576b	Transcription; Ionic Homeostasis; Cellular Organization;
YOR220W	577a	Unclassified Proteins;	YGL166W	577b	Transcription; Ionic Homeostasis; Cellular Organization;
YHL006C	578a	Unclassified Proteins;	YNL021W	578b	Transcription; Protein Destination; Cellular Organization;
YDL012C	579a	Unclassified Proteins;	YHR032W	579b	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;
YMR075C- A	580a	Unclassified Proteins;	YCR023C	580b	Transport Facilitation; Cell Rescue, Defense, Cell Death And Aging;
YGR113W	581a	Unclassified Proteins;	YGL061C	581b	Unclassified Proteins;
YGL061C	582a	Unclassified Proteins;	YDR016C	582a	Unclassified Proteins;
FUN11	583a	Unclassified Proteins;	YDR152W	583b	Unclassified Proteins;
YAL036C	584a	Unclassified Proteins;	YPL151C	584b	Unclassified Proteins;
FUN20	585a	Unclassified Proteins;	YHR207C	585b	Unclassified Proteins;
YAL032C	586a	Unclassified Proteins;	YIR044C	586b	Unclassified Proteins;
PKH1	587a	Unclassified Proteins;	YLR466W	587b	Unclassified Proteins;
YDR490C	588a	Unclassified Proteins;	YLR082C	588b	Unclassified Proteins;
PKH1	589a	Unclassified Proteins;	YJR050W	589b	Unclassified Proteins;
YDR490C	590a	Unclassified Proteins;	YGR129W	590b	Unclassified Proteins;
PKH1	591a	Unclassified Proteins;	YLR243W	591b	Unclassified Proteins;
SRL2	592a	Unclassified Proteins;	YMR255W	592b	Unclassified Proteins;
YLR082C	593a	Unclassified Proteins;	YDR078C	593b	Unclassified Proteins;
SYF1	594a	Unclassified Proteins;	YNL032W	594b	Unclassified Proteins;
YDR416W	595a	Unclassified Proteins;	YLR200W	595b	Unclassified Proteins;
SYF1	596a	Unclassified Proteins;	YCR030C	596b	Unclassified Proteins;
YDR416W	597a	Unclassified Proteins;	YFL002W-A	597b	Unclassified Proteins;
YHR016C	598a	Unclassified Proteins;	YJL162C	598b	Unclassified Proteins;
YSC84	599a	Unclassified Proteins;	YIL112W	599b	Unclassified Proteins;
YSC84	600a	Unclassified Proteins;	YLR35W	600b	Unclassified Proteins;
YHL006C	601a	Unclassified Proteins;	YHR140W	601b	Unclassified Proteins;
YNL056W	602a	Unclassified Proteins;	YDR183W	602b	Unclassified Proteins;
YFL023W	603a	Unclassified Proteins;	YEL068C	603b	Unclassified Proteins;
YAR031W	604a	Unclassified Proteins;	YFL017C	604b	Unclassified Proteins;
YBL101W-	605a	Unclassified Proteins;	YGR269W	605b	Unclassified Proteins;
A	606a	Unclassified Proteins;	YNL155W	606b	Unclassified Proteins;



YJR136C	Unclassified Proteins;
YKL090W	Unclassified Proteins;
YKR007W	Unclassified Proteins;
YKR022C	Unclassified Proteins;
YKR060W	Unclassified Proteins;
YKR083C	Unclassified Proteins;
YLR015W	Unclassified Proteins;
YLR065C	Unclassified Proteins;
YLR315W	Unclassified Proteins;
YLR328W	Unclassified Proteins;
YLR328W	Unclassified Proteins;
YLR424W	Unclassified Proteins;
YML119W	Unclassified Proteins;
YMR093W	Unclassified Proteins;
YNL056W	Unclassified Proteins;
YNL086W	Unclassified Proteins;
YNL091W	Unclassified Proteins;
YNL091W	Unclassified Proteins;
YNL091W	Unclassified Proteins;
YNL094W	Unclassified Proteins;
YNL122C	Unclassified Proteins;
YNR004W	Unclassified Proteins;
YNR029C	Unclassified Proteins;
YOL070C	Unclassified Proteins;
YOR023C	Unclassified Proteins;
YOR138C	Unclassified Proteins;
YOR215C	Unclassified Proteins;
YOR264W	Unclassified Proteins;
YOR264W	Unclassified Proteins;
YCR353C	Unclassified Proteins;
YPL110C	Unclassified Proteins;
YPL192C	Unclassified Proteins;
YPR105C	Unclassified Proteins;
YPR152C	Unclassified Proteins;
655a	Unclassified Proteins;
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655b	Unclassified Proteins;
656b	Unclassified Proteins;
657b	Unclassified Proteins;
658b	Unclassified Proteins;
659b	Unclassified Proteins;
660b	Unclassified Proteins;
661b	Unclassified Proteins;
662b	Unclassified Proteins;
663b	Unclassified Proteins;
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666b	Unclassified Proteins;
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689b	Unclassified Proteins;
690b	Unclassified Proteins;
691b	Unclassified Proteins;
692b	Unclassified Proteins;

In certain embodiments, the first polypeptide is labeled. In other embodiments, the second polypeptide is labeled, while in some embodiments, both the first and second polypeptides are labeled. Labeling can be performed using any art recognized method for labeling polypeptides. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

The invention also includes complexes of two or more polypeptides in which at least one of the polypeptides is present as a fragment of a complex-forming polypeptide according to the invention. For example, one or more polypeptides may include an amino acid sequence sufficient to bind to its corresponding polypeptide. A binding domain of a given first polypeptide can be any number of amino acids sufficient to specifically bind to, and complex with, the corresponding second polypeptide under conditions suitable for complex formation.

The binding domain can be the minimal number of amino acids required to retain binding affinity, or may be a larger fragment or derivative of the polypeptides listed in Table 3, columns 1 and 4. Procedures for identifying binding domains can be readily identified by one of ordinary skill in the art and the procedures described herein. For example, nucleic acid sequences containing various portions of a "bait" protein can be tested in a yeast two hybrid screening assay in combination with a nucleic acid encoding the corresponding "prey" protein.

In certain embodiments, the "bait" polypeptides of the complex are polypeptides categorized, for example, as a "Metabolism" protein in the MIPS database. In some embodiments, the "prey" protein of the complex is also a "Metabolism" protein, while in other embodiments the "prey" protein is, for example, an "Unclassified" protein (*see* Table 3; *e.g.*, ProPair 195a-310a and ProPair 195b-310b). Other MIPS categories include, *e.g.*, "Cell Growth/Cell Division/DNA Synthesis" proteins (*see* Table 2).

In other embodiments, the complexes are human ortholog complexes, chimeric complexes, or specific complexes implicated in fungal pathways, as discussed in detail below.

Polypeptides forming the complexes according to the invention can be made using techniques known in the art. For example, one or more of the polypeptides in the complex can be chemically synthesized using art-recognized methods for polypeptide synthesis. These methods are common in the art, including synthesis using a peptide synthesizer. See, e.g.,

- 5 *Peptide Chemistry, A Practical Textbook*, Bodansky, Ed. Springer-Verlag, 1988; Merrifield, *Science* 232: 241-247 (1986); Barany, et al, *Intl. J. Peptide Protein Res.* 30: 705-739 (1987); Kent, *Ann. Rev. Biochem.* 57:957-989 (1988), and Kaiser, et al, *Science* 243: 187-198 (1989).

Alternatively, polypeptides can be made by expressing one or both polypeptides from a nucleic acid and allowing the complex to form from the expressed polypeptides. Any known 10 nucleic acids that express the polypeptides, whether yeast or human (or chimerics of these polypeptides) can be used, as can vectors and cells expressing these polypeptides. Sequences of yeast ORFs and human polypeptides as referenced in Tables 3 and 7 are publicly available, e.g. at the Saccharomyces Genome Database (SGD) and GenBank (see, e.g. Hudson et al., *Genome Res.* 7: 1169-1173 (1997). If desired, the complexes can then be recovered and 15 isolated.

Recombinant cells expressing the polypeptide, or a fragment or derivative thereof, may be obtained using methods known in the art, and individual gene product or complex may be isolated and analyzed (See, e.g., e.g., as described in Sambrook et al., eds., MOLECULAR CLONING: A LABORATORY MANUAL, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold 20 Spring Harbor, NY, 1989; and Ausubel, et al., eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993). This is achieved by assays that are based upon the physical and/or functional properties of the protein or complex. The assays can include, e.g., radioactive labeling of one or more of the polypeptide complex components, followed by analysis by gel electrophoresis, immunoassay, cross-linking to marker-labeled 25 products. Polypeptide complex may be isolated and purified by standard methods known in the art (either from natural sources or recombinant host cells expressing the proteins/protein complex). These methods can include, e.g., column chromatography (e.g.. ion exchange, affinity, gel exclusion, reverse-phase, high pressure, fast protein liquid, etc), differential centrifugation, differential solubility, or similar methods used for the purification of proteins.

### 30 **Complexes Useful for Identifying Anti-Fungal Agents**

The invention further provides complexes of polypeptides useful, *inter alia*, in identifying agents that inhibit the growth of microorganisms such as fungi.

Human fungal infections have increased dramatically in incidence and severity in recent years. Advances in surgery and cancer treatments as well as the increasing use of broad-spectrum antimicrobials and the spread of HIV have increased the number of patients at risk for fungal infections. Most fungi are completely resistant to conventional antibacterial 5 drugs.

The antifungal drugs presently available fall into several categories depending on their mode of action, as discussed below. Because several complexes according to the invention include proteins associated with these modes of action, the complexes can be used to identify anti-fungal agents.

10 Protein interactions which are useful for identifying anti-fungal agents are considered below.

(i) *Interference In Nuclear Division*

15 Griseofulvin interferes with nuclear division in fungal mitosis by disrupting the mitotic spindle and inhibiting cytoplasmic microtubule aggregation by interacting with polymerized microtubules. There is evidence that griseofulvin binds to a microtubule-associated protein in addition to binding to tubulin.

In accordance with the present invention, several interactions have presently been identified where one of the interacting partners is a microtubule or a microtubule-associated protein. Inhibiting any of these interactions could lead to the disruption of microtubules and 20 interference in mitotic division, similar to the mode of action of griseofulvin, thereby providing a new means of inhibiting fungal activity. Accordingly, in some embodiments, the invention provides purified complexes of the proteins detailed in Table 4, below (interacting protein pairs are in bold, by row; a description of each protein follows).

**Table 4: Microtubule-related interactions identified**

<b>APG7</b> Apg12p-activating enzyme, involved in autophagy cytoplasm-to-vacuole protein targeting, and peroxisome degradation pathways	<b>AUT7</b> Forms a protein complex with Aut2p to mediate attachment of autophagosomes to microtubules. Aut7p has homology to LC3, a microtubule-associated protein from rat
<b>DUO1</b> Protein that interacts with Dam1p and causes cell death upon overproduction, involved in mitotic spindle function	<b>BIM1</b> Microtubule binding protein
<b>BUB3</b> Protein required for cell cycle arrest in response to loss of microtubule function	<b>MAD3</b> Checkpoint protein required for cell cycle arrest in response to loss of microtubule

	function
<b>KAR4</b> Regulatory protein required for pheromone induction of karyogamy genes, defective in nuclear fusion because of defect in microtubule-dependent movement of nuclei	<b>MUM2</b> Muddled Meiosis, mutant is sporulation defective and fails to perform premeiotic DNA synthesis
<b>CLN3</b> G1/S-specific cyclin that interacts with Cdc28p protein kinase to control events at START	<b>MAD3</b> Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
<b>EBS1</b> Protein with similarity to Est1p (Telomere elongation protein)	<b>MAD2</b> Spindle-assembly checkpoint protein
<b>MSB2</b> Protein for which overproduction suppresses bud emergence defect of cdc24 mutant, putative integral membrane protein	<b>MAD2</b> Spindle-assembly checkpoint protein
<b>MSB2</b> Protein for which overproduction suppresses bud emergence defect of cdc24 mutant, putative integral membrane protein	<b>MAD3</b> Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
<b>NUP157</b> Nuclear pore protein (nucleoporin)	<b>MAD2</b> Spindle-assembly checkpoint protein
<b>SAP4</b> Sit4p-associated protein (SIT4 is a protein phosphatase)	<b>MAD2</b> Spindle-assembly checkpoint protein
<b>SAP4</b> Sit4p-associated protein (SIT4 is a protein phosphatase)	<b>MAD3</b> Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
<b>SIN4</b> Component of RNA polymerase II holoenzyme/mediator complex, involved in positive and negative regulation of transcription, possibly via changes in chromatin structure	<b>MAD2</b> Spindle-assembly checkpoint protein
<b>SIN4</b> Component of RNA polymerase II holoenzyme/mediator complex, involved in positive and negative regulation of transcription, possibly via changes in chromatin structure	<b>MAD3</b> Checkpoint protein required for cell cycle arrest in response to loss of microtubule function
<b>YDR214W</b> Protein of unknown function	<b>MAD2</b> Spindle-assembly checkpoint protein
<b>YNL218W</b> Protein with similarity to <i>E. coli</i> DNA polymerase III gamma and tau subunits	<b>MAD2</b> Spindle-assembly checkpoint protein
<b>MCM16</b> Protein involved in chromosome segregation, plays a nonessential role that governs the kinetochore-microtubule mediated process of chromosome Segregation	<b>MCM22</b> Protein required for maintenance of chromosomes and minichromosomes
<b>CYP2</b> Cyclophilin (peptidylprolyl isomerase), ER or	<b>JSN1</b> Benomyl dependent tubulin mutant, Protein

secreted isoform, plays a role in the stress response	that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150
<b>SPC34</b> Protein component of the spindle pole body	<b>JSN1</b> Benomyl dependent tubulin mutant, Protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150
<b>YIL065C</b> Protein of unknown function	<b>JSN1</b> Benomyl dependent tubulin mutant, Protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150
<b>YLR392C</b> Protein of unknown function	<b>JSN1</b> Benomyl dependent tubulin mutant, Protein that when overexpressed can suppress the hyperstable microtubule phenotype of tub2-150

As described above, in certain embodiments of these complexes contain the binding domains, of the polypeptides recited in Table 4, while other embodiments contain conservative variants of these polypeptides, or polypeptides which contain the polypeptides recited in Table 4.

5                   (ii)     *Disruption of Ergosterol Biosynthesis*

Azoles are synthetic compounds that can be classified as imidazoles (ketoconazole, clotrimazole and miconazole) or triazoles (itraconazole and fluconazole). The antifungal activity of azole drugs result from their reduction in the biosynthesis of ergosterol, the main sterol in the cell membranes of fungi. Reduction of ergosterol alters the structure of the cytoplasmic membrane as well as the function of several membrane-bound enzymes (such as those involved in nutrient transport and chitin synthesis). The azole drugs reduce ergosterol synthesis by inhibiting the fungal cytochrome p450 enzymes, specifically they inhibit the sterol 14-alpha-demethylase, a microsomal cytochrome P450-dependent enzyme system, leading to a decrease in ergosterol and an accumulation of 14-alpha-methylsterols. There is some evidence that the primary target of the azoles is the heme protein, which cocatalyzes cytochrome P-450-dependent 14-alpha-dependent 14-alpha-demethylation of lanosterol. One interaction containing a heme biosynthesis protein has been presently been identified (Table 5). Disruption of this interaction could also lead to depletion of ergosterol and accumulation of sterol precursors, including 14-alpha-methylated sterols, forming a membrane with altered structure and function. Accordingly, in some embodiments, the invention provides a purified complex of the proteins recited in Table 5, below.

**Table 5: Heme biosynthesis protein interaction identified**

<b>SED1</b> Abundant cell surface glycoprotein that may contribute to cell wall integrity and stress resistance	<b>HEM13</b> Coproporphyrinogen III oxidase, oxygen-repressed, sixth step in heme biosynthetic pathway
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Complexes containing one or more variants of these polypeptides are within the scope of the present invention, as are polypeptides having amino acid sequences which include the 5 polypeptides recited in Table 5.

(iii) *Cell Wall Synthesis Inhibition*

Fungi share many biochemical targets with other eukaryotic cells. However, the fungal cell wall is a unique organelle and contains compounds, such as mannan, chitin and glucans, that are unique to fungi. The cell wall is dynamic and essential to the viability of the 10 fungi due to its roles in osmotic protection, transport of macromolecules, growth, conjugation and spore formation. Major disruption of the composition or organization of the cell wall deleteriously affects cell growth. A number of compounds have been discovered that inhibit the development of fungal cell walls. Two class of these antifungal drugs are echinocandins, which inhibit glucan synthesis, and nikkomycins, which inhibit chitin synthesis.

15 Several interactions between proteins localized to the cell wall or enzymes responsible for production of cell wall components have presently been identified. Inhibiting any of these interactions could lead to a disruption of the cell wall, hence providing new means for inhibiting fungal viability. Accordingly, in certain embodiments, the present invention provides purified complexes of the proteins detailed in Table 6, below.

20 **Table 6: Cell wall-related protein interactions identified**

<b>CDC11</b> Septin, component of 10 nm filaments of mother-bud neck; involved in cytokinesis	<b>SPR28</b> Septin-related protein expressed during sporulation
<b>YFR042W</b> Protein of unknown function	<b>KRE6</b> Glucan synthase subunit required for synthesis of beta-1,6-glucan, involved in cell wall beta-glucan assembly
<b>YDR482C</b> Protein of unknown function	<b>SCW11</b> Soluble cell wall protein
<b>SMI1</b> Protein involved in (1,3)-beta-glucan synthesis, possibly through regulation of cell wall glucan and chitin synthesis; Chromatin binding protein	<b>BAS1</b> Transcription factor regulating basal and induced activity of histidine and adenine biosynthesis genes

<b>WSC3</b> Protein required for maintenance of cell wall integrity and for the stress response	<b>PEX14</b> Peroxisomal peripheral membrane protein (peroxin) involved in import of peroxisomal matrix proteins
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Embodiments of these complexes containing the binding domains or conservative variants of these polypeptides are within the scope of the present invention, as are polypeptides which contain the polypeptides recited in Table 6.

## 5 Complexes Containing One or More Human Polypeptides

The invention also provides purified complexes of two or more human polypeptides. In some embodiments, the interacting polypeptides are human orthologs of the interacting yeast polypeptides. Human orthologs according to the invention are set out in Table 7, below.

Complexes of human ortholog binding domains, conservative variants, and 10 polypeptides including the human orthologs recited in Table 7, are within the scope of the invention, as are labeled ortholog complexes and/or polypeptides.

Table 7: Human ortholog protein interactions

Yeast accno (bait)	Human ortholog accno	Human ortholog name	Human ortholog description	Yeast accno (prey)	Human ortholog accno	Human ortholog name	Human ortholog description
yal032c	Q13573	SKIP	Nuclear protein Skip	yl1345w	p16118	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase/6PF-2,KIFRU-2,6-P2ase liver isozyme
yal032c	Q13573	SKIP	Nuclear protein Skip	yl1423c	q02224	CENPE	Centromeric protein E/CENPE protein
yal032c	Q13573	SKIP	Nuclear protein Skip	yl151c	p35606	COPP	Beta subunit of coatomer complex
yal034w-a	P06468	TPM2	Fibroblast muscle-type tropomyosin	yl172w	p49790	NUP153	Nuclear pore complex protein NUP153.
yal034w-a	P07951	TPM2	Skeletal beta-tropomyosin	yl172w	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein
yal034w-a	P35749	MYH11	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	yl172w	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP98
yal034w-a	P49454	CENPF	CENP-F kinetochore protein	yl172w	p23490	LOR	Loricrin
yal034w-a	Q15545	TAF2F	Transcription initiation factor TFIID 55 kD subunit	yl172w	p09651	HNRPA1	Heterogenous nuclear ribonucleoprotein A1/helix-destabilizing protein/single-strand binding protein/HNRNP core protein A1
yal034w-a	P06468	TPM2	Fibroblast muscle-type tropomyosin	ygr120c	p49454	CENPF	CENP-F kinetochore protein
yal034w-a	P07951	TPM2	Skeletal beta-tropomyosin	ygr120c	p30622	RSN	Restin
yal034w-a	P49454	CENPF	CENP-F kinetochore protein	ygr120c	p04114	APOB	Apolipoprotein B
-	yar003w	P78406	mRNP41	ybr175w	014727	APAF1	Apoptotic protease activating factor 1/APAF-1
49	yar003w	Q05048	CSTF1	ybr175w	p35606	COPP	Beta subunit of coatomer complex
-	yar003w	Q09028	RBAP48	ybr175w	q15542	TAFF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100
yar003w	Q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100	ybr175w	p04901	GNB1	Guanine nucleotide-binding protein G(i)/G(S)/G(T) beta subunit 1
yar003w	Q16576	RBBP7	Histone acetyl transferase type B subunit 2/retinoblastoma-binding protein Nucleolin/protein C23	ybr175w	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase 1B alpha subunit
yar014c	P19338	NCL	Sarcoplasmic reticulum histidine-rich calcium binding protein	yer133w	p37140	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit
yar014c	P23327	HRC	Cyclin I	yer133w	p08129	PPP1CA	Serine/threonine protein phosphatase PP1-alpha 1 catalytic subunit
yar014c	P35663	CYLC1	Transcriptional regulator ATRX/X-linked helicase II(X-linked nuclear protein	yer133w	p05323	PPP2CA	Serine/threonine protein phosphatase PP2A-alpha, catalytic subunit
yar014c	P46100	ATRX	Hypothetical protein KIAA0298	yer133w	p11082	PPP2CB	Amidoid-like protein 2/APPH/amyloid protein homolog
yb1101w-a	O15016	KIAA0298	Hypothetical protein KIAA0298	ybl043w	q06481	ALP2	Ankyrin, brain variant 1/ankyrin B
yb1101w-a	O15016	KIAA0298	Hypothetical protein KIAA0298	yfl002w-a	q01484	ANK2	DNAJ protein homolog 2/HSJ-2
yb1101w-a	O15016	KIAA0298	Hypothetical protein KIAA0298	yjl162c	p31689	HSJ2	Microtubule-associated protein 1B
yb1105c	P05127	PRKCB	Protein kinase C-beta-2/PKC-beta-2	ym1109w	p46821	MAP1B	Thyroid receptor interacting protein 12/KIAA0045
yb1105c	P17252	PRKCA	Protein kinase C alpha	ym1109w	q14669	TRIP12	60S acidic ribosomal protein P2
yb1006w	P30837	ALDH5	Mitochondrial aldehyde dehydrogenase X	ydr382w	p05387	RPLP2	

ybr006w	P00352	ALDH1	Aldehyde dehydrogenase, cytosolic/ALDH class 1/ALDH1/ALDH-E1	ykl023w	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type A/NMMHC-A	
ybr006w	P05091	ALDH2	Aldehyde dehydrogenase, mitochondrial/class 2/ALDH1/ALDH-E2	ykl023w	q08170	SFRS4	Pre-mRNA splicing factor SRp75	
ybr006w	P30837	ALDH5	Mitochondrial aldehyde dehydrogenase X	ykl023w	p35663	CYLC1	Cyclin I	
ybr006w	P47895	ALDH6	Aldehyde dehydrogenase 6	ykl023w	q14093	CYLC2	Cyclin II	
ybr006w	P49189	ALDH9	Aldehyde dehydrogenase, E3 isozyme/gamma-aminobutyraldehyde dehydrogenase	ykl023w	q14203	DCTN1	Dynactin, 150 kD isoform [fragment]	
ybr006w	P51649	SSADH	Succinate semialdehyde dehydrogenase/NAD+-dependent succinate-semialdehyde dehydrogenase	ykl023w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	
ybr103w	O14727	APAF1	Apoptotic protease activating factor 1/APAF-1	yil112w	p55273	CDKN2D	Cyclin-dependent kinase 4 inhibitor DP19INK4D	
ybr103w	P43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit	yil112w	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B	
ybr103w	Q15269	PWP2H	Periodic tryptophan protein 2 homolog	yil112w	q01485	ANK2	Brain ankyrin variant 2	
ybr103w	Q15542	TAF2D	Transcription initiation factor TFIID 100 kDa subunit/TAFI1-100/TAFII100	yil112w	p20749	BCL3	B-cell lymphoma 3-encoded protein	
ybr221c	P11177	PDHB	Pyruvate dehydrogenase E1-beta subunit	yli345w	q16875	F26P	6PF-2-K/FRU-2,6-P2ase brain/placenta-type bisphosphatase/6PF-2-K/FRU-2,6-P2ase liver isozyme	
ybr221c	P21953	BCKDHB	2-oxoisovalerate dehydrogenase beta subunit	yli345w	p16118	PFKFB1	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase/6PF-2-K/FRU-2,6-P2ase liver isozyme	
ybr221c	P51854	TKT2	Transketolase 2	yli345w	q16877	F263	6PF-2-K/FRU-2,6-P2ase testis-type isozyme/6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase	
50	ybr244w	P07203	GPX1	Glutathione peroxidase	yli117c	q14690	KIAA0185	RRP5 protein homolog KIAA0185 [fragment]
1	ybr244w	P18283	GPX2	Glutathione peroxidase-GI.	yli117c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	yli105c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit	
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	yir423c	q02224	CENPE	Centromeric protein E/CENP-E protein	
ybr270c	P30414	NKTR	NK-tumor recognition protein/Natural-killer cells cyclophilin-related protein	Ymr236w	q16594	TAF2G	Transcription initiation factorTFIID 31 kD subunit	
50	ybr274w	P53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	ylr258w	p34840	GYS2	Glycogen synthase, liver
1	ybr274w	P54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	ylr258w	p13807	GYS1	Muscle glycogen synthase
ybr274w	P27448	P78	Putative serine/threonine-protein kinase P78	Ymr255w	p46821	MAP1B	Microtubule-associated protein 1B	
ybr274w	P51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	Ymr255w	p29375	RBBP2	RBBP-2/retinoblastoma binding protein 2	
ybr274w	p53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	Ymr255w	q03111	ENL	ENL protein	
ybr274w	p54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	Ymr255w	p51825	MLLT2	AF-4 protein	
ybr274w	q14012	CAMK1	Calcium/calmodulin-dependent protein kinase type I	Ymr255w	p11387	TOP1	Topoisomerase I	
ybr274w	q15831	STK11	Serine/threonine-protein kinase 11	Ymr255w	p46939	UTRN	Urophin	

ycl020w	q15016	KIAA0298	Hypothetical protein KIAA0298	yfl002w-a	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B
ycl024w	p15735	PHKG2	Phosphorylase kinase, testis/liver, gamma-2	ykr048c	q01105	SET	Set protein/ HLA-DR associated protein II/PHAP II
ycl024w	p27448	P78	Putative serine/threonine-protein kinase P78	ykr048c	p46060	RANGAP1	RanGTPase activating protein 1
ycl024w	p53555	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	ykr048c	q99457	NAP1L3	Nucleosome assembly protein 1-like 3
ycl024w	p54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	ykr048c	p55209	NAP1L1	NAP-1/nucleosome assembly protein 1-like 1
ycl024w	q13131	PRKAA1	5'-AMP-activated protein kinase, catalytic alpha-1 chain	ykr048c	o15355	PPM1C	Protein phosphatase 2C gamma isoform/PP2C-GAMMA
ycl024w	q14012	CAMK1	Calcium/calmodulin-dependent protein kinase type I	ykr048c	q01534	TSPY	Homo sapiens testicular protein (TSPY) mRNA, complete cds.
ycl024w	q15831	STK11	Serine/threonine-protein kinase 11	ykr048c	p19338	NCL	Nucleosome assembly protein 2/nucleosome assembly protein 1-like 4
ycl024w	q16566	CAMK4	Calcium/calmodulin-dependent protein kinase IV	ykr048c	q99733	NAP1L4	Ryanodine receptor 1
ycl024w	q16816	PHKG1	Phosphorylase B kinase gamma catalytic chain, skeletal muscle isoform	ykr048c	p21817	RYR1	DNA replication licensing factor MCM2/KIAA0030
ycl059c	p46821	MAP1B	Microtubule-associated protein 1B	ygi201c	p49736	MCM2	Centromeric protein E/CENP-E protein
ycl065w	q05682	CALD1	Caldesmon/CDM	yhr123c	q02224	CENPE	Salivary proline-rich protein/cDNA CP3, CP4, and CP5
ycr009c	p15924	DSP	Desmoplakin I and II	ydr108w	p04280	PRB1	Atrophin-1/dentatorubral-pallidoluysian atrophy protein
ycr009c	p49418	AMPH	Amphiphysin	ydr108w	p54259	DRPLA	Proto-oncogene C-CRK
ycl006w	o15355	PPM1C	Protein phosphatase 2C gamma isoform/PP2C-GAMMA	ydr162c	p46108	CRK	Proto-oncogene tyrosine-protein kinase ABL/c-abl
-	p35813	PPM1A	Protein phosphatase 2C alpha	ydr162c	p00519	ABL1	Tyrosine-protein kinase BLK
-	p49593	KIAA0015	Putative protein phosphatase 2C/PP2C/KIAA0015	ydr162c	p51451	BLK	zinc finger protein 183
ycl012c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	ydr151c	o15541	ZNF183	Tristetraprolin/TTP/ZFP-36
-	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ydr151c	p26651	ZFP36	TIS11D protein/butyrate response factor 2/EGF-response factor 2
ycl012c	q10571	MN1	Possible global transcription activator MN1	ydr151c	p47974	BRF2	Tis11B protein/butyrate response factor 1/EGF-response factor 1
ycl012c	q93074	KIAA0192	Hypothetical protein KIAA0192	ydr151c	q07352	BRF1	Nicotinate-nucleotide pyrophosphorylase [carboxylating]/quinolinate phosphoribosyl transferase
ycl012c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	yfr047c	q15274	NADC	Thyroid receptor interacting protein 12/KIAA0045
ycl012c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	yor355w	q14669	TRIP12	
ycl012c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	yor355w	p42568	MLLT3	AF-9 protein
ycl013w	q07283	THH	Trichohyalin	ydr510w	p55854	SMT3H1	Ubiquitin-like protein SMT3A
ycl013w	q07283	THH	Trichohyalin	yer116c	p38398	BRCA1	BREAST CANCER, TYPE 1
ycl017w	p24941	CDK2	Cell division protein kinase 2	ycr050c	p49368	CCT3	T-complex protein 1, gamma subunit
ycl017w	p19784	CSNK2A2	Casein kinase II alpha'	ydl160c	p38919	NUK-34	Nuk-34 mRNA for translation initiation factor.
ycl017w	p24941	CDK2	Cell division protein kinase 2	ydl160c	q13838	BAT1	Probably ATP-dependent RNA helicase P47
ycl017w	q00526	CDK3	Cell division protein kinase 3	ydl160c	p04765	EIF4A1	Eukaryotic initiation factor 4A1
ycl017w	q00534	CDK6	Cell division protein kinase 6/PLSTIRE for serine/threonine protein kinase.	ydl160c	q14240	EIF4A2	Eukaryotic initiation factor 4AII
ycl017w	q00536	PCTK1	Serine/threonine protein kinase PC-TAIRE-1	ydl160c	p26196	DDX6	Probable ATP-dependent RNA helicase P54

ydi017w	p24941	CDK2	Cell division protein kinase 2	yj088w	p00480	OTC		
ydi074c	p11056	MYH3	Embryonic myosin heavy chain.	yjr423c	q15431	SYCP1	Ornithine carbamoyltransferase [precursor]/OTCase/cornithine transcarbamylase	
ydi074c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yjr423c	p12270	TPR	Synaptonemal complex protein 1/SCP-1 protein	
ydi074c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yjr423c	p30622	RSN	Nucleoprotein TPR	
ydi074c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	yjr423c	p05787	KRT8	Restin	
ydi074c	p15924	DSP	Desmoplakin I and II	yjr423c	p13535	MYH8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/Ck8	
ydi074c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yjr423c	p11047	LAMC1	Myosin heavy chain, perinatal skeletal muscle	
ydi074c	p49454	CENPF	CENPF kinetochore protein	yjr423c	p15924	DSP	Laminin gamma-1 chain [precursor]/laminin B2 chain	
ydi074c	q02224	CENPE	Centromeric protein E/CENP-E protein	yjr423c	p49454	CENPF	Desmoplakin I and II	
ydi074c	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1	yjr423c	q02224	CENPE	CENPF-F kinetochore protein	
ydi09c	p49356	FNTB	farnesyl-protein transferase beta-subunit	ykl019w	p49354	FNTA	Centromeric protein E/CENP-E protein	
ydi09c	p53609	PGGT1B	Geranylgeranyltransferase type I beta-subunit	ykl019w	q92696	RABGGTA	Protein farnesyltransferase alpha subunit	
ydi09c	q13098	GPS1	G protein pathway suppressor 1	yel009c	p05412	JUN	RAB geranylgeranyl transferase alpha subunit	
ydi13c	p15924	DSP	Desmoplakin I and II	yil036w	p35580	MYH10	Transcription factor AP-1/c-jun proto oncogene	
ydi113c	q02224	CENPE	Centromeric protein E/CENP-E protein	yil036w	p49454	CENPF	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	
ydi113c	p15924	DSP	Desmoplakin I and II	yil036w	p49454	CENPF	CENPF-F kinetochore protein	
ydi113c	q02224	CENPE	Centromeric protein E/CENP-E protein	yil036w	p49454	CENPF	CENPF-F kinetochore protein	
-	p05423	BN51T	BN51 protein	yil036w	q02224	CENPE	Centromeric protein E/CENP-E protein	
-	p06748	NPM1	Nucleophosmin	ykr025w	p39687	PHAP1	HLA-DR associated protein I	
-	p35663	CYLC1	Cyclin 1	ykr025w	o15355	PPM1C	Protein phosphatase 2C gamma isoform/PP2C-	
-	ydi150w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ykr025w	p46100	ATRX	GAMMA
-	ydi150w	p55081	MFAP1	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ykr025w	p21815	IBSP	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein
-	ydi150w	q14093	CYLC2	Microtubular protein 1	ykr025w	p19338	NCL	Bone sialoprotein II [precursor]/BSPII/Cell-binding sialoprotein
-	ydi150w	p43246	MSH2	Cylicin II	ykr025w	p17480	UBTF	Nucleolin/protein C23
ydi154w	p20585	MSH3	DNA mismatch repair protein MSH3	ygl025c	q02817	MUC2	1/UBF-1	
ydi154w	p43246	MSH2	DNA mismatch repair protein MSH2	ygl025c	q02078	MEF2A	Intestinal mucin 2/mucin 2	
ydi154w	p20585	MSH3	DNA mismatch repair protein MSH3	yil144w	p49454	CENPF	Myocyte-specific enhancer factor 2A	
ydi154w	p43246	MSH2	DNA mismatch repair protein MSH2	yil144w	q02224	CENPE	CENPF-F kinetochore protein	
ydi154w	p52701	MSH6	DNA mismatch repair protein MSH6/GT mismatch binding protein	yil144w	p15924	DSP	Centromeric protein E/CENP-E protein	
ydi154w	p43246	MSH2	DNA mismatch repair protein MSH2	yrm224c	p49959	MRE11A	Desmoplakin I and II	
ydi155w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ybr135w	p10275	AR	Double-strand break repair protein MRE11A/MRE11 homolog	
ydi203c	q14154	KIAA0141	Hypothetical protein KIAA0141	ygr058w	p28676	GCA	Androgen receptor	
ydi203c	q14154	KIAA0141	Hypothetical protein KIAA0141	ygr372c	p54259	DRPLA	Grancalcin	
ydi235c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yjr423c	q15431	SYCP1	Atrophin-1/identorubral-pallidoluysian atrophy protein	
ydi235c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yjr423c	p12270	TPR	Synaptonemal complex protein 1/SCP-1 protein	
							Nucleoprotein TPR	

yd1239c	p15924	DSP	Desmoplakin I and II	Yif423c	MYH8	Myosin heavy chain, perinatal skeletal muscle
yd1239c	p30622	RSN	Reslin	Yif423c	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
yd1239c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMHC-C-B	Yif423c	LAMC1	Laminin gamma-1 chain [precursor]/laminin B2 chain
yd1239c	p49454	CENPF	CENPF	Yif423c	DSP	Desmoplakin I and II
yd1239c	q02224	CENPE	Centromeric protein E/CENPF-E protein	Yif423c	CENPF	CENPF-F Kinetochoore protein
yd1239c	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1	Yif423c	CENPE	Centromeric protein E/CENPF-E protein
yd1239c	q08378	GOLGA3	Golgin-160	Yif423c	RSN	Reslin
yd1239c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	Yol091w	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
yd1239c	p15924	DSP	Desmoplakin I and II	Yol091w	TPR	Nucleoprotein TPR
yd1239c	p49454	CENPF	CENPF	Yol091w	EPS15	Epidermal growth factor receptor substrate 15
yd1239c	q02224	CENPE	Centromeric protein E/CENPF-E protein	Yol091w	CENPF	CENPF-F Kinetochoore protein
yd1239c	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1	Yol091w	CENPE	Centromeric protein E/CENPF-E protein
yd1239c	q08378	GOLGA3	Golgin-160	Yol091w	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type A/NMHC-A
yd1246c	p11766	ADH5	Class III alcohol dehydrogenase chI subunit	Yd1246c	ADH5	Class III alcohol dehydrogenase chI subunit
yd1246c	q00796	SORD	Sorbitol dehydrogenase/L-iditol-2 dehydrogenase	Yd1246c	SORD	Sorbitol dehydrogenase/L-iditol-2 dehydrogenase
yd1246c	p11766	ADH5	Class III alcohol dehydrogenase chI subunit	Yif159w	ADH5	Class III alcohol dehydrogenase chI subunit
yd1246c	q00796	SORD	Sorbitol dehydrogenase/L-iditol-2 dehydrogenase	Yif159w	SORD	Sorbitol dehydrogenase/L-iditol-2 dehydrogenase
yd0022w	p07197	NEFM	Neurofilament triplet M protein/160 kDa neurofilament protein/NF-M	Ykr048c	RYR1	Ryanodine receptor 1
-	p12036	NEFH	Neurofilament triplet H protein/200 kDa neurofilament protein	Ykr048c	SET	Set protein/ HLA-DR associated protein II/PHAPII
53	yd0022w	p35663	CYL1	Ykr048c	NAP1L1	NAP-1/nucleosome assembly protein 1-like 1
-	yd0022w	p43487	RANBP1	Ykr048c	RANGAP1	RanGTPase activating protein 1
yd0022w	p46821	MAP1B	Microtubule-associated protein 1B	Ykr048c	NAP1L3	Nucleosome assembly protein 1-like3
yd0022w	p49792	RANBP2	Nuclear pore complex protein NUP358/nucleoporin NUP358	Ykr048c	NAP1L4	Nucleosome assembly protein 2/nucleosome assembly protein 1-like 4
yd0022w	q92794	MOZ	Monocytic leukemia zinc finger protein	Ykr048c	TSPY	Homo sapiens testicular protein (TSPY) mRNA, complete cds.
yd0061w	p21439	MDR3	Membrane glycoprotein P	Ycr086w	CUTL1	CCAAT displacement protein/CDP
yd0077w	q02817	MUC2	Intestinal mucin 2/mucin 2	Ydr044w	CPO	Coprophorphyrinogen III oxidase/coprogen oxidase
yd0099w	p42655	YWHAE	14-3-3 protein epsilon	Ybl043w	APIP2	Amyloid-like protein 2/APPH/amylid protein homolog
yd0099w	p42655	YWHAE	14-3-3 protein epsilon	Ynl042w	DRPLA	Atrophin-1/dentatorubro-pallidoluysian atrophy protein
yd128w	o00628	PTS2R	Peroxisomal targeting signal 2 receptor	Ykl208w	RBAP48	Chromatin assembly factor 1 P48
yd128w	p35606	COPP	Beta subunit of coatomer complex	Ykl208w	GNB2-RS1	Subunit/retinoblastoma binding protein P48
yd128w	q09028	RBAP48	Chromatin assembly factor 1 P48	Yif208w	RBBP7	Guanine nucleotide-binding protein beta subunit-like protein 12.3
yd128w	q16376	RBBP7	Subunit/retinoblastoma binding protein P48	Yif208w	p43034	Histone acetyl transferase type B subunit
yd128w	q16376	RBBP7	Histone acetyl transferase type B subunit	Yif208w	PAFAH1B1	2/retinoblastoma-binding protein
			2/retinoblastoma-binding protein			Platelet-activating factor acetylhydrolase IB alpha subunit

ydr142c	p25388	GNB2-RS1	Guanine nucleotide-binding protein beta subunit-like protein 12.3	yil160c	p55084	HADHB	Trifunctional enzyme beta subunit, mitochondrial [precursor] ALPHA-METHYLACETOACETICACIDURIA
ydr142c	q09028	RBAP48	Chromatin assembly factor 1 P48 subunit/retinoblastoma binding protein P48	yil160c	p24752	AMLAD	
ydr142c	q13216	CKN1	Cockayne syndrome WD-repeat protein CSA	yil160c	p42765	THIM	3-ketoacyl-CoA thiolase mitochondrial/mitochondrial 3-oxacyl-CoA thiolase
ydr142c	q13610	PWP1	Periodic triptophan protein 1 homolog/keratinocyte protein IEF SSP 9502	yil160c	p22307	SCP2	Nonspecific lipid-transfer protein/sterol carrier protein 2
ydr142c	q16576	RBBP7	Histone acetyl transferase type B subunit 2/retinoblastoma-binding protein	yil160c	p09110	ACAA	Xsterol carrier protein 2 3-ketoacyl-CoA thiolase, peroxisomal/3-oxoacyl-CoA peroxisomal thiolase.
ydr148c	p10515	DLAT	Dihydroxyacetone acetyltransferase component of pyruvate dehydrogenase complex/PDC-E2	ydr510w	q93068	SMT3H3	Ubiquitin-like protein SMT3C
ydr148c	p11182	DBT	Lipoamide acyl transferase component of branched-chain alpha-keto acid dehydrogenase complex	ydr510w	p55855	SMT3H2	Ubiquitin-like protein SMT3B
ydr148c	p17677	GAP43	Neuromodulin/axonal membrane protein GAP-43	ydr510w	p55854	SMT3H1	Restin
ydr200c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	Ymr052w	p30622	RSN	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ydr200c	p49454	CENPF	CENPF kinase/kinetochore protein	Ymr052w	p35580	MYH10	Muscarinic acetylcholine receptor M3
ydr200c	p49454	CENPF	Nucleoprotein TPR	yil127w	p20309	CHRM3	CENPF kinase/kinetochore protein
ydr201w	p12270	TPR	Restin	yil144w	p49454	CENPF	Centromeric protein ECENP-E protein
ydr201w	p30622	RSN	Peanut-like protein 2/Brain protein H5	yil144w	q02224	CENPE	Septin 2 homolog [fragment]
54	043236	PNU1L2	Seplin 2 homolog [fragment]	yjr076c	q14141	KIAA0128	NEDD5 protein homolog/KIAA0158
-	ydr218c	KIAA0128	NEDD5 protein homolog/KIAA0158	yjr076c	q15019	NEDD5	Drebin E
-	ydr218c	q14141	CDC10 protein homolog	yjr076c	q16643	DBN1	CDC10 protein homolog
-	ydr218c	q15019	Histone H2A.1	yjr076c	q16181	CDC10	RANGAP1
-	ydr218c	NEDD5	Histone H2A.5	ykr048c	p46060	RANGAP1	Nucleosome assembly protein 1-like 3
-	ydr225w	CDC10	Histone H2A.X	ykr048c	q99457	NAP1L3	Nucleosome assembly protein 2/nucleosome assembly protein 1-like 4
-	ydr225w	H2AFA		ykr048c	q99733	NAP1L4	NAP1/nucleosome assembly protein 1-like 1
-	ydr225w	none		ykr048c	p55209	NAP1L1	CENPF kinase/kinetochore protein
-	ydr225w	p16104		ykr048c	p49454	CENPF	Centromeric protein ECENP-E protein
ydr225w	p28001	H2AFO	Histone H2A.2/H2A/O	ykr048c	q02224	CENPE	Myosin heavy chain, perinatal skeletal muscle
ydr228c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	yil423c	p13535	MYH8	Desmoplakin I and II
ydr228c	p54252	MJD1	Machado-Joseph disease protein 1	yil423c	p15924	DSP	Desmoplakin I and II
ydr228c	q10571	MN1	Probable tumor suppressor protein MN1	yil423c	p15924	DSP	CENPF kinase/kinetochore protein
ydr228c	q93074	KIAA0192	Hypothetical protein KIAA0192	yil423c	p49454	CENPE	Centromeric protein ECENP-E protein
ydr259c	p11055	MYH3	Embryonic myosin heavy chain.	yil423c	q02224	NASP	Nuclear autoantigenic sperm protein
ydr259c	p15924	DSP	Desmoplakin I and II	yil423c	p49321	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
ydr259c	p49454	CENPF	CENPF kinase/kinetochore protein	yil423c	p35580		Apolipoprotein B
ydr308c	p24928	POLR2A	DNA-directed RNA polymerase II largest subunit.	yil174w			Centromeric protein ECENP-E protein
ydr308c	q03001	BPAG1	Bullous 230 kDa pemphigoid antigen 1	yil174w			
ydr311w	p32780	BTF2	Basic transcription factor 62kD subunit	ygr120c	p04114	APOB	
ydr311w	p32780	BTF2	Basic transcription factor 62kD subunit	yil423c	q02224	CENPE	

ydr320c	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	yf003w	p35606	COPP	Beta subunit of coatomer complex
ydr320c	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1	yf003w	q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100
ydr320c	p19338	NCL	Nucleolin/protein C23	yf003w	p04901	GNB1	Guanine nucleotide-binding protein G(I)(G(S)Y/G(T) beta subunit 1
ydr320c	p34991	TCEB1L	Cyclin A/CDK2-associated p19	yf003w	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit
ydr376w	p22570	FDXR	NADPH:adrenodoxin oxidoreductase [precursor]/adrenodoxin reductase/ferredoxin-NADP+ reductase	ycrf03w	p54252	MJD1	Machado-joseph disease protein 1
ydr376w	p22570	FDXR	NADPH:adrenodoxin oxidoreductase [precursor]/adrenodoxin reductase/ferredoxin-NADP+ reductase	yf024c	p49321	NASP	Nuclear autoantigenic sperm protein
ydr388w	p14317	HCLS1	Hematopoietic lineage cell specific protein	ycrd09c	p15924	DSP	Desmoplakin I and II
ydr388w	p49418	AMPH	Amphiphysin	ycrd09c	p49418	AMPH	Amphiphysin
ydr394w	p17980	PSMC3	26S protease regulatory subunit 6A/TAT-binding protein 1/TBP-1	ygr232w	q06547	E4TF1B	GA binding protein beta-1 chain
ydr394w	p35998	PSMC2	26S protease regulatory subunit 7/MSS1 protein	ygr232w	q01485	ANK2	Brain ankyrin variant 2
ydr394w	p43686	PSMC4	26S protease regulatory subunit 6BTAT-binding protein-7/TBP-7	ygr232w	p53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1
ydr394w	p47210	PSMC5	26S proteasome regulatory subunit 8/proteasome subunit p45	ygr232w	p20749	BCL3	B-cell lymphoma 3-encoded protein
1 ydr394w	q03527	PSMC1	26S protease (S4) regulatory subunit	ygr232w	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B
5 ydr394w	q92524	PSMC6	26S protease regulatory subunit S10B/proteasome subunit P42	ygr232w	p42773	CDN2C	Cyclin dependent kinase 6 inhibitor
1 ydr408c	p22102	GART	Trifunctional purine biosynthetic protein adenosine-3' trifunctional purine biosynthetic protein adenosine-3'	ygr053w	p41223	EDG2	G10 protein homolog
5 ydr408c	p22102	GART	yor174w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	
ydr416w	q14690	KIAA0185	RRP5 protein homolog/KIAA0185 [fragment]	ygr129w	q02224	CENPE	Centromeric protein E/CENP-E protein
ydr429c	p33240	CSTF2	Cleavage stimulation factor, 64 KD subunit	yf0117c	p08578	SNRPE	Small nuclear ribonucleoprotein E/snRNP-E
ydr439w	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	ycrf06w	p3986w	CUTL1	CCAA1 displacement protein/CDP
ydr477w	p54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	yef027c	p10451	SPP1	Osteopontin [precursor]
ydr482c	p42566	EPS15	Epidermal growth factor receptor substrate 15	ygl028c	q02505	MUC3	Mucin 3 [fragments]/intestinal mucin 3
ydr482c	q02224	CENPE	Centromeric protein ECENP-E protein	ygl028c	q02817	MUC2	Intestinal mucin 2/mucin 2
ydr490c	p17612	PRKACA	cAMP-dependent protein kinase catalytic subunit type alpha	yf1466w	q02505	MUC3	Mucin 3 [fragments]/intestinal mucin 3
yer018c	p02546	LMN1	Lamin C	yhr193c	p50502	HIP	Progesterone receptor-associated p48 protein
yer018c	p02545	LMN1	Lamin A/70 KD Lamin	Ymr117c	p30622	RSN	Restin
yer018c	p02546	LMN1	Lamin C	Ymr117c	p49454	CENPF	CENP-F kinetochore protein
yer018c	p35749	MYH11	Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	Ymr117c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
yer018c	q07283	THH	Trichohyalin	Ymr117c	p11055	MYH3	Embryonic myosin heavy chain.
yer018c	q93074	KIAA0192	Hypothetical protein KIAA0192	Ymr117c	p42566	EPS15	Epidermal growth factor receptor substrate 15
yer023w	p32322	PYCR1	Pyrrolidine 5-carboxylate reductase	yer023w	p32322	PYCR1	Pyrrolidine 5-carboxylate reductase

yer082c	p11016	GNB2	Guanine nucleotide-binding protein beta subunit 2 40S ribosomal protein S8 40S ribosomal protein S8 Origin recognition complex subunit 2	ykl142w ybr135w yfl017c ycr036w ydr299w ydr299w	p07942 p10275 p08578 p09880 p19338 p46060 p07197	LAMB1 AR SNRPE CUTL1 NCL RANGAP1 NEFM	Laminin beta-1 chain/laminin B1 chain Androgen receptor Small nuclear ribonucleoprotein EsnRNP-E CCAAT displacement protein/CDP Nucleolin/protein C23 RanGTPase activating protein 1 Neurofilament triplet M protein/160 Kd neurofilament protein/NF-M
yer102w	p09058	RPS8	Restin				
yer102w	p09058	RPS8	Cyclin I				
q13416	ORC2L		Myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]				
yer108w	p30622	RSN	Transcriptional regulator ATRX/X-linked helicase III/X-linked nuclear protein	ydr299w	p21817	RYR1	Transcriptional regulator ATRX/X-linked helicase III/X-linked nuclear protein
yer127w	p35663	CYLC1	Ankyrin, brain variant 1/ankyrin B	ydr299w	p46100	ATRX	Calreticulin/52kD ribonucleoprotein autoantigen RO/SS-A
yer127w	p35749	MYH11	Ribosomal protein S26	yfl435w	p27797	CALR	Replication factor C large subunit/activator 1140 Kd subunit
yer127w	p46100	ATRX	Serine/threonine protein phosphatase PP2A-alpha, catalytic subunit	ynl233w	p35251	RFC1	Cyclin I
yer127w	q01484	ANK2	Serine/threonine protein phosphatase PP1-alpha 1	ynl233w	p35663	CYLC1	AF-4 protein
yer131w	q06722	RPS26	Serine/threonine protein phosphatase PP2A-beta, catalytic subunit	ynl233w	p51825	MLLT2	Microtubule-associated protein 1B
yer133w	p05323	PPP2CA	Serine/threonine protein phosphatase PP1-beta 1	ynl233w	p46821	MAP1B	Dek protein
yer133w	p08129	PPP1CA	Serine/threonine protein phosphatase PP2A-beta, catalytic subunit	ynl233w	p35659	DEK	Phosphorylase B kinase gamma catalytic chain, skeletal muscle isoform
yer133w	p11032	PPP2CB	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	ynl233w	p15735	PHKG2	Serine/threonine-protein kinase NEK3 [fragment]
yer133w	p36873	PPP1CC	Probable ubiquitin carboxyl-terminal hydrolase FAF-Y	ybr059c	q16816	PHKG1	Map kinase-activated protein kinase MAPKAPK2
yer133w	p37140	PPP1CB	Ubiquitin carboxyl-terminal hydrolase 5/isopeptidase T	ybr059c	p51956	NEK3	Serine/threonine-activated protein kinase 2
yer144c	o00507	FAF-Y	Ubiquitin C-terminal hydrolase 11	ybr059c	p49137	NEK2	Serine/threonine-protein kinase NEK2
yer144c	p45974	USP5	Queoine tRNA-ribosyl transferase/tRNA-quanine transglycosylase	ybr059c	p51955	PAK2	Phosphorylase kinase, testis/liver, gamma-2
yer144c	p51784	USP11	Intestinal mucin 2/mucin 2	ybr059c	q13177	PAK2	Serine/threonine-protein kinase PAK-gamma
yer144c	p54578	USP14	Ubiquitin carboxyl-terminal hydrolase 13/isopeptidase T-3	ybr059c	p27448	P78	Putative serine/threonine-protein kinase P78
yer144c	q02817	MUC2	Probable ubiquitin carboxyl-terminal hydrolase FAF-X associated ubiquitin-specific protease	ybr059c	p51957	STK2	Serine/threonine-protein kinase NRK2
yer144c	q92995	USP13	DNA repair protein RAD51	yer179w	q06609	RAD51	DNA repair protein RAD51
yer144c	q93008	USP9X	Ubiquitin carboxyl-terminal hydrolase 7/herpesvirus	ybr059c	q14565	DMC1	Mitotic recombination protein DMC1/LIM15 homolog
yer144c	q93009	USP7	associated ubiquitin-specific protease	yer179w	p29354	GRB2	Salivary proline-rich protein/Clone CP7
yer179w	q06609	RAD51	Salivary proline-rich protein/clone CP3, CP4, and CP5	ygr136w	p06241	FYN	Salivary proline-rich protein/clone CP3, CP4, and CP5
yer179w	q14565	DMC1	Salivary proline-rich protein PO [fragment]/allele M	ygr136w	p14317	HCL1S1	Salivary proline-rich protein PO [fragment]/allele K
yfl010c	p02812	PRB2	Salivary proline-rich protein CP7	ygr136w	p19878	NCF2	Neutrophil cytosol factor 2/NCF-2/neutrophil NADPH oxidase factor 2/P67-PHOX
yfl010c	p04280	PRB1	Salivary proline-rich protein CP3, CP4, and CP5	ygr136w			Monocytic leukemia zinc finger protein
yfl010c	p10161	PRB4	Salivary proline-rich protein CP3, CP4, and CP5	ygr136w			
yfl010c	p10162	PRB4	Salivary proline-rich protein CP3, CP4, and CP5	ygr136w			
yfl010c	p17600	SYN1	Synapsin I/brain protein 4.1	ygr136w	q92794	MOZ	

yf010c	p22670	RFX1	MHC class II regulatory factor RFX1	ygr136w	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17
yf010c	p23246	PSF	PTB-associated splicing factor	ygr136w	p16333	NCK	Cytoplasmic protein NCK
yf010c	p35637	FUS	RNA-binding protein FUS/TLS	ygr136w	p46108	CRK	Proto-oncogene C-CRK
yf010c	q92793	CREBBP	CREB-BINDING PROTEIN	ygr136w	p07947	YES1	Proto-oncogene tyrosine-protein kinase YES/C-YES
yf010c	q92794	MOZ	Monocytic leukemia zinc finger protein	ygr136w	p15498	VAV	Vav proto-oncogene
yf010c	q98217	AIH1	AMELOGENESIS IMPERFECTA 1, HYPOPLASTIC TYPE	ygr136w	p46109	CRKL	Crk-like protein
yf010c	p02812	PRB2	Salivary proline-rich protein/Clone CP7	yor197w	p02812	PRB2	Salivary proline-rich protein/clone CP3, CP4, and CP5
yf010c	p04280	PRB1	Salivary proline-rich protein/clone CP3, CP4, and CP5	yor197w	p04280	PRB1	Salivary proline-rich protein/clone CP3, CP4, and CP5
yf010c	p10161	PRB4	Salivary proline-rich protein PO [fragment]allele M	yor197w	p54253	SCA1	Ataxin-1/Spinocerebellar ataxia type 1 protein
yf010c	p22670	RFX1	MHC class II regulatory factor RFX1	yor197w	q09472	EP300	E1A-associated protein P300
yf010c	p23246	PSF	PTB-associated splicing factor	yor197w	q93074	KIAA0192	Hypothetical protein KIAA0192
yf010c	p35637	FUS	RNA-binding protein FUS/TLS	yor197w	p42858	HD	Huntingtin/huntington's disease protein
yf010c	q99217	AIH1	AMELOGENESIS IMPERFECTA 1, HYPOPLASTIC TYPE	yor197w	q01844	EWSR1	RNA-binding protein EWS
yf023w	q02224	CENPE	Centromeric protein ECENP-E protein	ybr154c	p19388	POLR2E	DNA-directed RNA polymerase II 23 kD polypeptide/RPB25/XAP4
yf023w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/N/M/H/C-B	ytl200w	p49454	CENPF	CENPF kinetochore protein
yf023w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ytl200w	q08379	GOLGA2	Golgin-95
-	yf023w	NES	Nestin	ytl200w	p42566	EPS15	Epidermal growth factor receptor substrate 15
-	yf023w	CENPE	Centromeric protein ECENP-E protein	ytl200w	q02224	CENPE	Centromeric protein ECENP-E protein
yf024c-a	p14317	HCLS1	Hematopoietic lineage cell specific protein	ybl007c	q99102	MUC4	Tracheo-bronchial mucin 4/mucin 4 [fragment]
yf024c-a	p16333	NCK	Cytoplasmic protein NCK	ybl007c	p16333	NCK	Cytoplasmic protein NCK
yf024c-a	p29354	GRB2	Growth factor receptor-bound protein 2	ybl007c	p29354	GRB2	Growth factor receptor-bound protein 2
yf024c-a	p41240	CSK	Tyrosine-protein kinase CSK	ybl007c	p06241	FYN	Proto-oncogene tyrosine-protein kinase FYN/SYN
yf024c-a	p46109	CRKL	Crk-like protein	ybl007c	p09769	M19722	Human fgr proto-oncogene encoded p55-c-fgr protein, complete cds.
yf024c-a	p98171	RGC1	RHO-GAP hematopoietic protein C1	ybl007c	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17
yf024c-a	q13813	SPTA2	Spectrin alpha chain, brain/honeytrroid alpha-spectrin	ybl007c	p07947	YES1	Proto-oncogene tyrosine-protein kinase YES/C-YES
yf024c-a	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17	ybl007c	q14687	KIAA0182	Hypothetical protein KIAA0182
yf024c-a	p46109	CRKL	Crk-like protein	ygr28c	q92794	MOZ	Monocytic leukemia zinc finger protein
yf047c	q15274	NADC	Nicotinate-nucleotide pyrophosphorylase [carboxylating]/quinolinolate phosphoribosyl transferase	yhd047c	q15274	NADC	Nicotinate-nucleotide pyrophosphorylase [carboxylating]/quinolinolate phosphoribosyl transferase
ygl058w	p23567	UBE2B	Ubiquitin-conjugating enzyme E2-17 kD	ycr056w	q00755	PML	Probable transcription factor PML
ygl058w	p47986	UBE2B3	Ubiquitin-conjugating enzyme E2-17 kD 3	ycr056w	p35227	MEL18	DNA-binding protein MEL-18/Zinc finger protein 144
ygl058w	p49459	UBE2A	Ubiquitin-conjugating enzyme E2-17 kD/HR6A	ycr056w	p15918	RAG1	V(D)J recombination activating protein 1
ygl058w	p50550	UBE2I	Ubiquitin conjugating enzyme E2-18 kD	ycr056w	015541	ZNF183	zinc finger protein 183
ygl058w	p51668	UBE2D1	Ubiquitin conjugating enzyme E2-17 kD	ycr056w	p35226	BMI1	DNA-binding protein BMI1
ygl058w	p51669	UBE2D2	Ubiquitin conjugating enzyme E2-17 kD 2	ycr056w	p38398	BRCA1	BREAST CANCER, TYPE 1
ygl058w	p51985	UBE2E1	Ubiquitin conjugating enzyme E2-21 kD UBCH6	ycr056w	p29591	PML	Probable transcription factor PML

yg1058w	p56554	UBE2G2	Ubiquitin-conjugating enzyme E2 G2	ycr066w	p29592	PML
yg1058w	q16781	UBE2N	Ubiquitin-conjugating enzyme E2-17 kD	ycr066w	p29590	Probable transcription factor PML
yg1058w	UBE2G1	TAF2E	Ubiquitin-conjugating enzyme E2 G1	ycr066w	p29593	Probable transcription factor PML
yg1112c	p49848	TAF2E	Transcription initiation factor TFIID 70 kD subunit/TAFII-70	Ymt236w	q16594	Transcription initiation factor TFIID 31 kD subunit
yg1112c	p49848	TAF2E	Transcription initiation factor TFIID 70 kD subunit/TAFII-70	Ymt255w	p51825	AF-4 protein
yg115W	p54619	PRKAG1	5'-AMP-activated protein kinase, gamma-1 subunit	yer027c	p10451	Osteopontin [precursor]
yg112c	p42858	HD	Huntington/huntington's disease protein	ykr026c	q14232	Translation initiation factor eIF-2B alpha subunit
yg112c	q14814	MEF2D	Myocyte-specific enhancer factor 2D	ykr026c	p49770	Translation initiation factor EIF-2B beta subunit/S20lil15
yg150c	o14647	CHD2	Chromodomain-helicase-DNA-binding protein 2/CHD-2	ydl002c	p17480	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1
yg150c	p19338	NCL	Nucleolin/protein C23	ydl002c	p36402	T-cell-specific transcription factor 1/TCF-1
yg150c	p28370	SMARCA1	Possible global transcription activator SNF2L1	ydl002c	q00059	Mitochondrial transcription factor 1
yg150c	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ydl002c	TCF6L1	High mobility group protein HMG2/HMG-2
yg150c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ydl002c	p26583	Structure-specific recognition protein 1
yg150c	p51532	SMARCA4	Possible global transcription activator SNF2L4/BRG-1 protein	ydl002c	SOX4	High mobility group-1 protein
yg150c	q03468	CSB	Excision repair protein ERCC-6/cockayne syndrome protein CSB	ydl002c	q08945	Transcription factor SOX-4
yg150c	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	yor355w	q09429	High mobility group-1 protein
yg150c	q03468	CSB	Excision repair protein ERCC-6/cockayne syndrome protein CSB	yor355w	q14669	Thyroid receptor interacting protein 12/KIAA0045
yg150c	q03468	CSB	farnesylation-protein transferase beta-subunit	ykl019w	p42568	TRIP12
yg155w	p49336	FNTB	Geranylgeranylyltransferase type I beta-subunit	ykl019w	p49354	AF-9 protein
yg155w	p53699	PGGT1B	Phosphorylase kinase, testis/liver, gamma-2	ykl019w	q92696	Protein farnesyltransferase alpha subunit
yg158w	p15735	PHKG2	Putative serine/threonine-protein kinase P78	yrl113w	RABGGTA	RAB geranylgeranyl transferase alpha subunit
yg158w	p27448	P78		yrl113w	p53779	Mitogen-activated protein kinase 10
yg158w	p49137	MAPKAPK-2	Map kinase-activated protein kinase 2	yrl113w	p53778	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6
yg158w	p49137	MAPKAPK-2	Map kinase-activated protein kinase 2	yrl113w	p27361	Mitogen-activated protein kinase 3/extracellular signal-regulated kinase 1
yg158w	p51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	yrl113w	q15759	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 1
yg158w	p53355	DAPK1	Death-associated protein kinase 1	yrl113w	p23482	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2
yg158w	q14012	CAMK1	Calcium/calmodulin-dependent protein kinase I	yrl113w	q16539	Mitogen-activated protein kinase 14/CSBP
yg158w	q16566	CAMK4	calcium/calmodulin-dependent protein kinase IV	yrl113w	q13164	Mitogen-activated protein kinase 7/ERK5
yg158w	q16816	PHKG1	Phosphorylase B kinase gamma catalytic chain, skeletal muscle isoform	yrl113w	p45984	Mitogen-activated protein kinase 9
yg189c	q06722	RPS26	Ribosomal protein S26	yrl435w	p27797	Calreticulin/52kD ribonucleaseprotein autoantigen RO/SS-A
yg192w	p04062	GBA	Glucosylceramidase	ybl057c	p49454	CENPF

ygj237c	p23511	NFYA	CAAT-box DNA binding protein subunit B	ybl021c	p25208	NFYB	CCAAT-binding transcription factor subunit A/CAAT-box DNA binding protein subunit B
ygj237c	p54259	DRPLA	Atrophin-1/dentatorubral-pallidoluysian atrophy protein	ybl021c	q01658	DR1	TATA binding protein subunit B
ygj242c	p20749	BCL3	B-cell lymphoma 3-encoded protein	ykr099w	p10244	MYBL2	Myb-related protein B/B-myb
ygj242c	p53355	DAPK1	Death-associated protein kinase 1/DAP-kinase 1	ykr099w	p10242	MYB	MYB proto-oncogene protein
ygj242c	q01484	ANK2	Ankyrin, brain variant 1/ankyrin B	ykr099w	p25024	APC	Adenomatous polyposis coli protein
ygj242c	q01485	ANK2	Brain ankyrin variant 2	ykr099w	p10243	MYBL1	Myb-related protein AA-myb
ygj254w	p08151	GLI1	GL1 protein/zinc finger protein GLI1	ygr047c	p19338	NCL	Nucleolin/protein C23
ygj254w	p41182	BCL6	B-cell lymphoma 6 protein/zinc finger protein 51	ygr047c	p51531	SMARCA2	Possible global transcription activator SNF2/L2/BRM
ygj254w	p41182	BCL6	B-cell lymphoma 6 protein/zinc finger protein 51	yord39w	p13862	CSNK2B	Casein kinase II beta subunit
ygj2764	q92764	KRTHA5	Keratin, type I cuticular HA5/hair keratin, type I HA5	ygr010w	q92764	KRTHA5	Keratin, type I cuticular HA5/hair keratin, type I HA5
ygj010w	p35558	NUP214	Nuclear pore complex protein NUP214/CAN protein	yil144w	p15924	DSP	Desmoplakin I and II
ygj014w	q02817	MUC2	Intestinal mucin 2/mucin 2	yil144w	q02224	CENPE	Centromeric protein E/CENP-E protein
ygj014w	q14157	KIAA0144	Hypothetical protein KIAA0144	yil144w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform
ygj014w	q99102	MUC4	Tracheobronchial mucin 4/mucin 4 [fragment]	yil144w	p49454	CENPF	CENP-F kinetochore protein
ygj017w	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1	yil403w	q92785	REQ	Zinc-finger protein UBF-D4/apoptosis response zinc finger protein requiem
ygj058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	ygr058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase
ygj058w	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit	ygr058w	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit
ygj058w	p20807	CAPN3	Calpain 94, large [catalytic] subunit/calcium activated	ygr058w	p20807	CAPN3	Calpain P94, large [catalytic] subunit/CANP
59	p28676	GCA	Grancalcin	ygr058w	p28676	GCA	Grancalcin
ygj058w	p30526	SRI	Sorcin	ygr058w	p30626	SRI	Sorcin
ygj058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	ygr136w	p46108	CRK	Proto-oncogene C-CRK
-	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit	ygr136w	p06241	FYN	Proto-oncogene tyrosine-protein kinase FYN/SYN
ygj058w	p20807	CAPN3	Calpain 94, large [catalytic] subunit/calcium activated	ygr136w	p29354	GRB2	Growth factor receptor-bound protein 2
ygj058w	p28676	GCA	Grancalcin	ygr136w	p46109	CRKL	Crk-like protein
ygj058w	p30526	SRI	Sorcin	ygr136w	p14317	HCLS1	Hematopoietic lineage cell specific protein
ygj058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	yil113w	q13164	MAPK7	Mitogen-activated protein kinase 7/ERK5
ygj058w	p17655	CAPN2	Ca2-activated neutral proteinase/calpain 2, Large [catalytic] subunit	yil113w	p53778	MAPK12	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6
ygj058w	p20807	CAPN3	Calpain 94, large [catalytic] subunit/CANP	yil113w	p45984	MAPK9	Mitogen activated protein kinase 9
ygj058w	p28676	GCA	Grancalcin	yil113w	p28482	MAPK1	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2
ygj058w	p30626	SRI	Sorcin	yil113w	p53779	MAPK10	Mitogen-activated protein kinase 10
ygj058w	p07384	CAPN1	Calpain 1, large [catalytic] subunit/calcium activated neutral proteinase	ynt047c	q92636	NSMAF	Protein fyn/factor associated with n-smase activation
ygj058w	p28676	GCA	Grancalcin	ynt047c	q99418	ARNO	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor

ygr108w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ybr135w	p10275	AR	Androgen receptor
ygr119c	p23490	LOR	Loricrin	ygl1172w	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein
ygr119c	p35637	FUS	RNA-binding protein FUS/TLS	ygl1172w	p49790	NUP153	Nuclear pore complex protein NUP153.
ygr119c	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein	ygl1172w	p09651	HNRPA1	Heterogeneous nuclear ribonucleoprotein A1/helix-
							destabilizing protein/single-strand binding
							protein/HNRNP core protein A1
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	ygl1172w	p23490	LOR	Loricrin
ygr119c	p49790	NUP153	Nuclear pore complex protein NUP153.	ygl1172w	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP
ygr119c	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin	ygl1172w	p13645	KRT10	98
ygr119c	p23490	LOR	Loricrin	yj041w	q14093	CYLC2	Cytlin II
ygr119c	p35637	FUS	RNA-binding protein FUS/TLS	yj041w	p35663	CYLC1	Cytlin I
ygr119c	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein	yj041w	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	yj041w	p37198	NUP62	Nuclear pore glycoprotein P62
ygr119c	p49790	NUP153	Nuclear pore complex protein NUP153.	yj041w	p49790	NUP153	Nuclear pore complex protein NUP153.
ygr119c	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin	yj041w	p52948	NUP98	Nuclear pore complex protein NUP98/Nucleoporin NUP
							98
ygr119c	p23490	LOR	Loricrin	yjr423c	p15924	DSP	Desmoplakin I and II
ygr119c	p35637	FUS	RNA-binding protein FUS/TLS	yjr423c	p49454	CENPF	CENPF, kinetochore protein
ygr119c	p35658	NUP214	Nuclear pore complex protein NUP214/CAN protein	yjr423c	p30622	RSN	Reslin
-	ygr119c	p37198	NUP62	yjr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
-	ygr119c	p49790	NUP153	yjr423c	p13535	MYH8	Myosin heavy chain, perineal skeletal muscle
-	ygr119c	p52948	NUP98	yjr423c	p12270	TPR	Nucleoporin TPR
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	Ymr236w	q16594	TAFF2G	Transcription initiation factor TFIIID 31 kD subunit
ygr144w	q16134	ETFDH	Electron transfer flavoprotein-ubiquinone	ygr144w	q16134	ETFDH	Electron transfer flavoprotein-ubiquinone
			oxidoreductase				oxidoreductase
ygr155w	p35520	CBS	Cystathione beta-synthase	ycr086w	p39880	CUTL1	CCAAT displacement protein/CDP
ygr229c	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase III-X-linked nuclear protein	ycr095w	p10243	MYBL1	Myo-related protein AA-myb
ygr119c	p37198	NUP62	Nuclear pore glycoprotein P62	ykr099w	p25054	APC	Adenomatous polyposis coli protein
ygr144w	q16134	ETFDH	Electron transfer flavoprotein-ubiquinone	ykr099w	p10242	MYB	MYB proto-oncogene protein
			oxidoreductase	ykr099w	p10244	MYBL2	Myb-related protein BB-myb
				yin001c	p26378	ELAVL4	Paraneoplastic encephalomyelitis antigen 3
ygr155w	p35520	CBS	Cystathione beta-synthase	yin001c	q01844	EWSR1	RNA-binding protein EWS
ygr229c	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase III-X-linked nuclear protein	yin001c	p35637	FUS	RNA-binding protein FUS/TLS
				yin001c	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit
				yin001c	q01085	TIAL1	Nucleolysin TIAR
ygr229c	p46821	MAP1B	Microtubule-associated protein 1B	yir001c	p11940	PABPL1	PolyA binding protein 1
ygr229c	q05682	CALD1	Caldesmon/CDM	yir001c	p08621	SNRP70	U1 small nuclear ribonucleoprotein 70kD
ygr229c	q07283	THH	Trichohyalin	yir001c	p98179	RBPM3	Putative RNA binding protein 3
ygr250c	p11940	PABPL1	PolyA binding protein 1				
ygr250c	p26378	ELAVL4	Paraneoplastic encephalomyelitis antigen 3				
ygr250c	p29558	RBMS1	Single-stranded DNA binding protein MSSP-1				
ygr250c	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit				
ygr250c	p38159	HNRPG	Heterogeneous nuclear ribonucleoprotein G/H/NRNP				
			Glycoprotein P3				
			Putative RNA binding protein 3				
			Nucleolysin TIAR				
			Spliceosome associated protein 49SAP49				

ygr267c	<b>GCH1</b>	GTP cyclohydrolase I	ygr267c	<b>GCH1</b>	GTP cyclohydrolase I
yhr004w	<b>LAMR1</b>	Colon carcinoma laminin-binding protein	yil423c	<b>CENPE</b>	Centromeric protein E/CENP-E protein
yhr018w	<b>PCBD</b>	Plerin-4-alpha-carbinolamine dehydratase	yhi018w	<b>PCBD</b>	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE
yhr019c	<b>CLAPM1</b>	Clathrin coat assembly protein AP50/KIAA0109 gene	yki135c	<b>CLAPB1</b>	Beta adaptin
yhr019c	<b>P47B</b>	Clathrin coat assembly protein AP47 homolog 2	yki135c	<b>ADTB1</b>	Beta-adaptin 1
yhr021w	<b>P48047</b>	Transcription factor SP1 [fragment]	yil056c	<b>p52745</b>	Zinc finger protein 36/zinc finger protein K0X12
yhr021w	<b>SP1</b>	GLI protein/zinc finger protein GLI1	yil056c	<b>ZNF36</b>	Zinc finger protein 132
yhr021w	<b>GLI1</b>	Tax helper protein 2/zinc finger protein GLI2	yil056c	<b>ZNF132</b>	Zinc finger protein 133
yhr021w	<b>GLI2</b>	Zinc finger protein GLI3	yil056c	<b>ZNF133</b>	Zinc finger protein 135
yhr021w	<b>GLI3</b>	Early growth response protein 2/EGR-2	yil056c	<b>ZNF146</b>	Zinc finger protein OZF
yhr021w	<b>EGR2</b>	Early growth response protein 1	yil056c	<b>ZNF239</b>	Zinc finger protein 239/HOK-2
yhr021w	<b>EGR1</b>	Wilm's tumor protein/WT33	yil056c	<b>ZNF31A</b>	Zinc finger protein 37A [fragment]
yhr021w	<b>WT1</b>	Zinc finger protein 43/Zinc protein HTF6	yil056c	<b>ZNF177</b>	Zinc finger protein 177
yhr021w	<b>ZNF43</b>	Transcription factor SP4/SPPR-1	yil056c	<b>ZNF157</b>	Zinc finger protein 157
yhr021w	<b>SP4</b>	Early growth response protein 4	yil056c	<b>ZNF33A</b>	Zinc finger protein 33A/KIAA0065
yhr021w	<b>EGR4</b>	Early growth response protein 3	yil056c	<b>ZNF145</b>	Zinc finger protein PLZF/Zinc finger protein 145
yhr021w	<b>EGR3</b>	Proto-oncogene tyrosine-protein kinase FYN/SYN	Ymr255w	<b>ENL</b>	ENL protein
yhr016c	<b>FYN</b>	Hematopoietic lineage cell specific protein	Ymr255w	<b>RBBP2</b>	RBBP-2/retinoblastoma binding protein 2
yhr016c	<b>HCLS1</b>	Cytoplasmic protein NCK	Ymr255w	<b>TOP1</b>	Topoisomerase I
yhr016c	<b>NCK</b>	Growth factor receptor-bound protein 2	Ymr255w	<b>MAP1B</b>	Microtubule-associated protein 1B
yhr016c	<b>GRB2</b>	Tyrosine-protein kinase CSK	Ymr255w	<b>MLLT2</b>	AF-4 protein
-	<b>CSK</b>	Spectrin alpha chain, brain/honey thyroid alpha-spectrin	Ymr255w	<b>CHD2</b>	Chromodomain-helicase-DNA-binding protein 2/CHD-2
yhr016c	<b>SPTA2</b>	Intersectin/SH3 domain-containing protein SH3P17	Ymr255w	<b>UTRN</b>	Utrrophin
yhr016c	<b>ITSN</b>	Mitochondrial aldehyde dehydrogenase X	ydr480w	<b>LGALS3</b>	Galectin-3/gE-binding protein
yhr039c	<b>ALDH5</b>	Proteasome subunit C9	ydr447c	<b>ATP6E</b>	Vacuolar ATP synthase subunit AC39
yhr060w	<b>PSMA4</b>	DNA-directed RNA polymerase II largest subunit.	ydr480w	<b>LGALS3</b>	Galectin-3/gE-binding protein
yhr084w	<b>POLR2A</b>	Bullous 230 kDa pemphigoid antigen 1	yhr423c	<b>CENPE</b>	Centromeric protein E/CENP-E protein
yhr108w	<b>BPAG1</b>	Ubiquitin activating enzyme E1	yhr111w	<b>UBE1</b>	Ubiquitin activating enzyme E1 homolog
yhr111w	<b>UBE1</b>	Ubiquitin-activating enzyme E1 homolog	yhr111w	<b>UBE1L</b>	Ubiquitin-activating enzyme E1 homolog
yhr111w	<b>UBE1L</b>	C-FES/FPS proto-oncogene tyrosine-protein kinase	yhr423c	<b>CENPF</b>	CENPF kinetochore protein
yhr114w	<b>FES</b>	FES/FPS	yhr423c	<b>KRT8</b>	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
yhr114w	<b>TPR</b>	Nucleoprotein TPR	yhr423c	<b>MYH8</b>	Myosin heavy chain
yhr114w	<b>MYH7</b>	Myosin heavy chain, cardiac muscle beta isoform	yhr423c	<b>DSP</b>	Desnoplakin I and II
yhr114w	<b>HCLS1</b>	Hematopoietic lineage cell specific protein	yhr423c	<b>RSN</b>	Restin
yhr114w	<b>NCK</b>	Cytoplasmic protein NCK	yhr423c	<b>CENPE</b>	Centromeric protein E/CENP-E protein
yhr114w	<b>FER</b>	Tyrosine kinase FER	yhr423c	<b>TPR</b>	Nucleoprotein TPR
yhr114w	<b>RGC1</b>	RHO-GAP hematopoietic protein C1	yhr423c	<b>LAMC1</b>	Laminin gamma-1 chain [precursor]/laminin B2 chain
yhr114w	<b>CTTN</b>	SRC substrate contactin/amplaxin	yhr423c	<b>SYCP1</b>	Synaptonemal complex protein 1/SCP-1 protein
yhr114w	<b>ITSN</b>	Intersectin/SH3 domain-containing protein SH3P17	yhr423c	<b>CENPE</b>	Centromeric protein E/CENP-E protein
yhr143w-a	<b>POLR2K</b>	DNA-directed RNA polymerases I, II, and III 7.0 KD polypeptide	yhr423c	<b>NCL</b>	Nucleolin/protein C23
yhr171w	<b>UBE1</b>	Ubiquitin activating enzyme E1	ymr007c	<b>p19338</b>	NCL
61	<b>p22314</b>	Ubiquitin activating enzyme E1	ymr007c	<b>p19338</b>	NCL

Ribosomal protein L30							
yrh204w	p23908	MA12	Mannosyl-oligosaccharide alpha-1,2-mannosidase	ygi030w	RPL30		
yrh204w	p45844	ABC G1	White protein homolog	ydr174w	HMG1	High mobility group-1 protein	
yrh204w	p56545	CTBP2	C-terminal binding protein 2	phg0429	CTBP2	C-terminal binding protein 2	
yrh204w	p56545	CTBP1	C-terminal binding protein 1	p56545	CTBP1	C-terminal binding protein 1	
yrh204w	q13363	CTBP1	C-terminal binding protein 1	q13363	CTBP2	C-terminal binding protein 2	
yrh204w	q13363	CTBP2	C-terminal binding protein 2	q13363	CTBP1	C-terminal binding protein 1	
yrh204w	q13363	CTBP1	C-terminal binding protein 1	q14565	DMC1	Mitotic recombination protein DMC1/LIM15 homolog	
yrh204w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID			DNA repair protein RAD51	
yrh204w	q93074	KIAA0192	Hydrolytic protein KIAA0192	yer179w	RAD51	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor	
yrh204w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	ynl047c	ARNO	Protein fan/factor associated with n-smase activation	
yrh204w	q93074	KIAA0192	Hydrolytic protein KIAA0192	ynl047c	NSMAF	Cyclin I	
yrh204w	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit	ygi174w	CYLC1	Restin	
yrh204w	p08670	VIM	Vimentin	yfr423c	p30622	Desmoplakin I and II	
yrh204w	p12882	MYSS	Myosin heavy chain skeletal muscle, light meromyosin region	yfr423c	p15924	CENPF	
yrh204w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, smooth muscle isoform/SMMHC [FRAGMENT]	yfr423c	p19454	TPR	Nucleoprotein TPR
yrh204w	p35749	MYH11	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yfr423c	p12270		
yrh204w	p48681	NES	Nestin	yfr423c	p15535	NYH8	Myosin heavy chain, perinatal skeletal muscle
yrh204w	p49454	CENPF	CENPF-F kinetochore protein	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yrh204w	q15036	KIAA0064	Hypothetical protein KIAA0064	yfr423c	q15431	SYCP1	Synaptonemal complex protein 1/SSCP-1 protein
yrh204w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yfr510w	p55854	SMT3H1	Ubiquitin-like protein SMT3A
yrh204w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yfr423c	p42568	MLLT3	AF-9 protein
yrh204w	p35769	GATA2	Endothelial transcription factor GATA-2	yfr423c	q13547	HDAC1	Histone deacetylase 1/HD1
yrh204w	p23771	GATA3	Trans-acting T-cell specific transcription factor GATA-3	yfr423c	q92769	HDAC2	Histone deacetylase 2/HD2
yrh204w	yj110c	GATA4	Transcription factor GATA-4	ynl021w	0153179	DHA3	Histone deacetylase 3
yrh204w	yj110c	GATA6	Transcription factor GATA-6	ynl021w	p56524	KIAA0288	Hypothetical protein KIAA0288
yrh204w	yj112w	GNB2	Guanine nucleotide-binding protein beta subunit 2	ynl001w	q05193	Dynamin-1	Dynamin-1
yrh204w	yj112w	p43034	PAFAH1B1	ynl001w	p20591	DNM1	Interferon-regulated resistance GTP-binding protein
yrh204w	yj112w	TAF110	Platelet-activating factor acetylhydrolase IB alpha subunit	ynl001w	p20592	MX1	MXA/Interferon-induced protein P78
yrh204w	yj112w	SAZD	WD-repeat protein SAZD	ynl001w	p50570	Dynamin-2	Interferon-regulated resistance GTP-binding protein
yrh204w	yj112w	TAF2D	Transcription initiation factor TFIID 100 kDa subunit/TAFI-100/TAFII100	ynl001w	MX2	MXB	
yrh204w	yj137c	GYG	Glycogenin-1	yil137c	p46976	GYG	Glycogenin-1
yrh204w	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	ydr311w	p32780	BTF2	Basic transcription factor 6/2D subunit
yrh204w	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	yk0622w	p29084	GTF2E2	Transcription factor IIE beta subunit
yrh204w	o00746	NME4	Nucleoside-diphosphate kinase	yk067w	000746	NME4	Nucleoside-diphosphate kinase A
yrh204w	p15531	NME1	Nucleoside-diphosphate kinase A	yk067w	p15531	NME1	Nucleoside-diphosphate kinase A

yk1067w	p22392	NME2	Nucleoside diphosphate kinase B/NDP kinase B/nm23-H2	yk1067w	p22392	NME2	Nucleoside diphosphate kinase B/NDP kinase B/nm23-H2
yk1142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain	yk1142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain
yk1142w	p07942	LAMB1	Laminin beta-1 chain/Laminin B1 chain	Ymr165c	p51825	MLLT2	AF-4 protein
yk1166c	p14619	PRKG1	Type I beta cGMP-dependent protein kinase	yil033c	p10644	PRKAR1A	cAMP-dependent protein kinase regulatory subunit type I-alpha
yk1166c	p17612	PRKACA	cAMP-dependent protein kinase catalytic subunit type I alpha	yil033c	q16281	CNGC3	CNG3/cyclic nucleotide-gated cation channel 3 [fragment]
yk1166c	p22694	PRKACB	Testis-specific cAMP-dependent protein kinase catalytic subunit C-beta isoform	yil033c	q14028	CNG4	Cyclic-nucleotide-gated cation channel 4
yk1166c	p23443	RPS6KB1	P70 ribosomal S6 kinase alpha-II	yil033c	p29973	CNGC1	CGMP-gated cation channel protein/cyclic nucleotide-gated channel photoreceptor/cyclic nucleotide-gated cation channel 1/CNG channel 1/CNG1/CNG-1
yk1166c	p24723	PRKCH	Protein kinase C, ETA type/protein kinase C-L	yil033c	p31321	PRKAR1B	cAMP-dependent protein kinase regulatory subunit RI-beta
yk1166c	p31749	AKT1	RAC-alpha serine/threonine kinase	yil033c	p13861	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory chain
yk1166c	p31751	AKT2	RAC-beta serine/threonine kinase	yil033c	p31323	PRKAR2B	cAMP-dependent protein kinase subunit RI-beta
yk1166c	p51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	yil033c	p14619	PRKG1	Type I beta cGMP-dependent protein kinase
-	yk026c	EIF2B2	Translation initiation factor EIF-2B beta subunit/S20 <i>iii</i> 15	yk026c	p49770	EIF2B2	Translation initiation factor EIF-2B beta subunit/S20 <i>iii</i> 15
63	yk026c	ELF2B1	Translation initiation factor EIF-2B alpha subunit	yk026c	q14232	ELF2B1	Translation initiation factor EIF-2B alpha subunit
-	yk037c	EPS15	Epidermal growth factor receptor substrate 15	yd1201w	p30622	RSN	Reslin
-	yk083c	HMG1	High mobility group-1 protein	yk052c	p19338	NCL	Nucleolin/protein C23
yk083c	p17480	UBTF	Nucleolar transcription factor I/upstream binding factor 1/UBF-1	yk052c	q92794	MOZ	Monocytic leukemia zinc finger protein
yk046c	p33240	CSTF2	Cleavage stimulation factor, 64 kD subunit	yrf047c	q15274	NADC	Nicotinate-nucleotide pyrophosphorylase [carboxylating]/quinolinolate phosphoribosyl transferase
yk200w	p49454	CENPF	CENPF	Ymr052w	p30622	RSN	Reslin
yk200w	q02224	CENPE	Centromeric protein E/CENP-E protein	Ymr052w	p35580	MYH10	Myo5in heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
yk1216c	p05092	CYP4	Peptidyl-prolyl cis-trans isomerase A/cyclophilin A	yi037w	p36969	GPX4	Phospholipid hydroperoxide glutathione peroxidase/PHGPX
yk1216c	p23284	PPIB	Peptidyl-prolyl CIS-trans Isomerase B	yi037w	p18283	GPX2	Glutathione peroxidase-GI.
yk1216c	p30405	CYP3	Iprecursor/cyclophilin B	yi037w	p12079	GPRP	Glutathione peroxidase-related protein 1
yk1216c	p45877	PPIC	Peptidyl-prolyl CIS-Trans isomerase/cyclophilin C	yi037w	p22352	GPX3	Plasma glutathione peroxidase
yk1216c	q08752	PPID	Peptidyl-prolyl cis-trans isomerase C/cyclophilin C	yi037w	p07203	GPX1	Glutathione peroxidase
yk1229c	p21181	CDC42	40 kD peptidyl-prolyl CIS-TRANS isomerase/cyclophilin-40 mRNA, complete cds.	yd1135c	p52565	ARHGDA	Rho GDP-dissociation Inhibitor 1.
yk1229c	p25763	CDC42	G25K GTP-binding protein G25K, placental isoform	yd1135c	p52566	ARHGDI	Rho GDP-dissociation inhibitor 2.
yk1245c	p32320	CDA	GTP-binding protein G245c	yd1245c	p32320	CDA	Cytidine deaminase
yk12336	p42336	PIK3CA	Cytidine deaminase	yor355w	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045

1	yf305c	p42345	FRAP	isoform	FKBP-rapamycin associated protein	ygr355w	p42568	MLT3	AF-9 protein
	yf423c	p15924	DSP	Desmoplakin I and II		ygr120c	p30622	RSN	Restin
	yf423c	p49454	CENPF	CENPF	Kinetochoore protein	ygr120c	p49454	CENPF	CENPF
	yf423c	q02224	CENPE	Centromeric protein E/CENP-E protein		ygr120c	p04114	APOB	Apolipoprotein B
	yf423c	p05787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8		yfr423c	p03787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin 8/K8/CK8
	yf423c	p11047	LMC1	Laminin gamma-1 chain [precursor]laminin B2 chain		yfr423c	p11047	LMC1	Laminin gamma-1 chain [precursor]laminin B2 chain
	yf423c	p12270	TPR	Nucleoprotein TPR		yfr423c	p12270	TPR	Nucleoprotein TPR
	yf423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle		yfr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
	yf423c	p15924	DSP	Desmoplakin I and II		yfr423c	p15924	DSP	Desmoplakin I and II
	yf423c	p30622	RSN	Restin		yfr423c	p30622	RSN	Restin
	yf423c	p49454	CENPF	CENPF	Kinetochoore protein	yfr423c	p49454	CENPF	CENPF
	yf423c	q02224	CENPE	Centromeric protein E/CENP-E protein		yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein
	yf423c	q15431	SYCP1	Synaptonemal complex protein 1/SYCP-1 protein		yfr423c	q15431	SYCP1	Synaptonemal complex protein 1/SYCP-1 protein
	yf424w	p49454	CENPF	CENPF	Kinetochoore protein	ykr022c	p49454	CENPF	CENPF
	yf424w	p52756	LUCA15	Putative tumor suppressor LUCA15		ykr022c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
	yf424w	p98175	DXS8237E	DXS8237E protein		ykr022c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
	yf429w	p31146	CORO1	Coronin-like Protein p57		ydr328c	p07199	CENP-B	Major centromere autoantigen B/centromere protein B
	yf429w	p43034	PFAFH1B1	Platelet-activating factor acetylhydrolase 1B alpha subunit		ydr328c	p34991	TCEB1L	Cyclin A/CDK2-associated p19
	yf429w	p46821	MAP1B	Microtubule-associated protein 1B		ydr328c	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1
2	yf429w	q16576	RBBP7	Histone acetyl transferase type B subunit 2/retinoblastoma-binding protein		ydr328c	p19338	NCL	Nucleolin/protein C23
3	yf432w	p12268	IMPDH2	Inosine monophosphate dehydrogenase 2		ydr167w	q12962	TAF2H	Transcription initiation factor TFIID 30 kDa subunit/TAFI-30/TAFII30
4	yf432w	p12268	IMPDH2	Inosine monophosphate dehydrogenase 2		ydr167w	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit
5	yf432w	p12268	IMPDH1	Inosine-5'-monophosphate dehydrogenase 1/IMP dehydrogenase 1/IMPDH-1/IMPD		ykr026c	p49770	EIF2B2	Translation initiation factor eIF-2B beta subunit/S20lii15
6	yf432w	p20839	PPP2CA	Serine/threonine protein phosphatase PP2A-alpha, catalytic subunit		yfr047c	q99418	ARNO	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor
7	yf433c	p05323	PPP3CA	Serine/threonine protein phosphatase 2B catalytic subunit. Alpha isoform/carmodulin-dependent calcineurin A subunit, alpha subunit		yfr047c	q92636	NSMAF	Protein fan/factor associated with n-smase activation
8	yf433c	q08209	PPP3CA	Ornithine aminotransferase		ygr010w	q92764	KRTHAS	Keratin, type I cuticular HAS/hair keratin, type I HA5
	yf438w	p04181	OAT	Ornithine aminotransferase		yho025w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID
	yf438w	p04181	OAT	Transcription initiation factor IIA alpha and beta chains/TFIIA-42		ydr167w	q12962	TAF2H	Transcription initiation factor TFIID 30 kDa subunit/TAFI-30/TAFII30
	ym015c	p52655	GTF2A1	Transcription initiation factor IIA alpha and beta chains/TFIIA-42		ydr174w	p09429	HMG1	High mobility group-1 protein
	ym015c	q15544	TAF2I	Transcription initiation factor TFIID 28 kDa subunit		ydr174w	p26583	HMG2	High mobility group protein HMG2/HMG-2

ymr088w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	ydr328c	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	
ymr094w	p49454	CENPF	CENP-F kinetochore protein	ylr200w	q02224	CENPE	Centromeric protein E/CENP-E protein	
ymr094w	q98471	MM-1	C-myc binding protein MM-1	ylr200w	p49454	CENPF	CENP-F kinetochore protein	
ymr114c	q02832	BLSA	B-lymphocyte antigen/B-lymphocyte surface antigen	ydr167w	q12962	TAF2H	Transcription initiation factor TFIID 30 kDa subunit/TAFII-30/TAFII30	
ymr032w	p02533	KRT14	Keratin, type I cytoskeletal 14	ylr423c	p49454	CENPF	CENP-F kinetochore protein	
ymr032w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	ylr423c	q02224	CENPE	Centromeric protein E/CENP-E protein	
ymr052w	p30622	RSN	Reslin	ylr005w	p12270	TPR	Nucleoprotein TPR	
ymr052w	p35580	MYH10	Myosin heavy chain, type B/cellular myosin heavy chain, type B/NMHC-C-B	ylr005w	q02224	CENPE	Centromeric protein E/CENP-E protein	
ymr068w	p20749	BCL3	B-cell lymphoma 3-encoded protein	yil105c	q10571	MN1	Probable tumor suppressor protein MN1	
ymr068w	q01484	ANK2	Ankyrin, brain variant /ankyrin B	yil105c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	
ymr068w	q01485	ANK2	Brain ankyrin variant 2	yil105c	q93074	KIAA0192	Hypothetical protein KIAA0192	
ymr077c	p12270	TPR	Nudeoprotein TPR	yk1052c	p19338	NCL	Nucleolin/protein C23	
ymr077c	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type A/NMHC-A	yk1052c	q92794	MOZ	Monocytic leukemia zinc finger protein	
ymr091c	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	ydr307c	q15431	SYCP1	Synaptonemal complex protein 1/SYCP-1 protein	
ymr093w	q14727	APAF1	Apoptotic protease activating factor 1/APAF-1	ydr398w	p17480	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/UBF-1	
ymr093w	p25388	GNB2-RS1	Guanine nucleotide-binding protein beta subunit-like protein 12.3	ylr398w	p07199	CENP-B	Major centromere autoantigen B/centromere protein B	
ymr093w	p35606	COPP	Beta subunit of coatomer complex	ylr398w	p27824	CANX	Calnexin/IP90	
ymr093w	q13610	PWP1	Periodic triptophan protein 1 homolog/keratinocyte protein IEF SSP 9502	ylr398w	p39687	PHAP1	HLA-DR associated protein I	
-	ymr093w	q15542	TAF2D	Transcription initiation factor TFIID 100 kDa subunit/TAFII-100/TAFII100	ylr398w	q01105	SET	Set protein/ HLA-DR associated protein II/PHAPII
6	ymr093w	p25388	GNB2-RS1	Guanine nucleotide-binding protein beta subunit-like protein 12.3	ynl218w	p35249	RFC4	Activator 1 37 kDa subunit/replication factor C, 37-kDa
5	ymr093w	q15542	TAF2D	Transcription initiation factor TFIID 100 kDa subunit/TAFII-100/TAFII100	ynl218w	p35250	RFC2	Activator 1 40 kDa subunit/replication factor C, 40 kDa
ymr102c	p25388	PAFAH1B1	Guanine nucleotide-binding protein beta subunit-like protein 12.3	ynl218w	p40937	RFC5	Activator 1 36 kDa subunit/replication factor C, 36-kDa	
ymr102c	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB alpha subunit	ynl218w	p35251	RFC1	Replication factor C large subunit/activator 1140 kDa subunit	
ymr102c	p53621	COPA	Coatomer alpha subunit	ynl218w	p35251	RFC1	Laminin beta-1 chain/Laminin B1 chain	
ymr102c	q13610	PWP1	Periodic triptophan protein 1 homolog/keratinocyte protein IEF SSP 9502	ylr1218w	p07942	LAMB1	Centromeric protein E/CENP-E protein	
ymr120w	p08910	PHS1-2	PHS1-2 with ORF homologous to membrane receptor proteins	ylk1142w	q02224	CENPE	Monocytic leukemia zinc finger protein	
ymr212c	q14156	KIAA0143	Hypothetical protein KIAA0143	ylr423c	q92794	MOZ	Hypothetical protein KIAA0192	
ymr255w	q14647	CHD2	Chromodomain-helicase-DNA-binding protein 2/CHD-2	yg1122c	p20226	TBP	TATA-binding protein/transcription activator SNF2L2/BRM	
ymr255w	p11387	TOP1	Topoisomerase I	yg1122c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	
ymr255w	p28375	RBBP2	RBBP-2/retinoblastoma binding protein 2	yg1122c				
ymr255w	p46821	MAP1B	Microtubule-associated protein 1B	yg1122c				

ymr255w	p46939	UTRN	Utrrophin	ygi122c	q10571	MN1	Probable tumor suppressor protein MN1	
ymr255w	p51825	MLLT2	AF-4 protein	ygi122c	p42858	HD	Huntingtin/huntington's disease protein	
ymr255w	q03111	ENL	ENL protein	ygi122c	q14814	MEF2D	Myocyte-specific enhancer factor 2D	
ymr255w	q15181	PP	Inorganic pyrophosphatase [fragment]/PPase	ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit	
ymr257w	q15663	CYLC1	Cyclin I	ykr026c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit	
ymr269w	p35580	CYLC2	Cyclin II	ykr026c	p49770	EIF2B2	Translation initiation factor EIF-2B beta subunit/S20lii/15	
ymr269w	q14093	UBTF	Nucleolar transcription factor 1/upstream binding factor 1/JBF-1	ynl047c	q92636	NSMAF	Protein fam/factor associated with n-snase activation	
ymr309c	p17480		Myosin heavy chain, nonmuscle type B/cellular	ynl047c	q99418	ARNO	ARF nucleotide-binding site opener/ARNO protein/ARF exchange factor	
ymr309c	p35580	MYH10	myosin heavy chain, type B/NMMHC-B	ynl047c	p41567	SU1	Protein translation factor SU11 homolog/sui1iso1	
ymr309c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular	ynl244c				
ymr309c	p1023c	FBN1	myosin heavy chain, type B/NMMHC-B	Yml224c	p49959	MRE11A	Double-strand break repair protein MRE11A/MRE11 homolog	
ymr309c	p35555		Fibrillin 1 [precursor]	Yml224c	p55209	NAP1L1	NAP1/nucleosome assembly protein 1-like 1	
ymr309c	p18583	SON	Son protein/son3	ykr048c	q13190	STX5A	Syntaxin 5	
ymr309c	q02832	BLSA	B-lymphocyte antigen/B-lymphocyte surface antigen	ynl164c	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045	
ymr309c	p46821	MAP1B	Microtubule-associated protein 1B	yor355w	p42568	MLLT3	AF-9 protein	
ymr309c	q02832	BLSA	B-lymphocyte antigen/B-lymphocyte surface antigen	yor355w	p20265	POU3F2	Nervous-system specific octamer-binding transcription factor N-Oct 3/N-Oct 5a/N-Oct 5b	
ymr309c	p23327	HRC	Sarcoplasmic reticulum histidine-rich calcium binding protein	yp1229w				
ymr309c	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular	yp1229w	p15131	SMARCA2	Possible global transcription activator SNF2/2/BRM	
ymr309c	p35749	MYH11	myosin heavy chain, type A/NMMHC-A	yp1229w	q93074	KIAA0192	Hypothetical protein KIAA0192	
ymr309c	p45379	TNNT2	[FRAGMENT]	yp1229w	q01826	SATB1	DNA binding protein SATB1	
ymr309c	p46100	ATRX	Triontin T, cardiac muscle isoforms	yp1229w	p54252	MJD1	Machado-joseph disease protein 1	
ymr309c	ymr309c		Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	yp1229w				
ymr309c	p46821	MAP1B	Microtubule-associated protein 1B	yp1229w	p42858	HD	Huntingtin/huntington's disease protein	
ymr309c	q02832	BLSA	B-lymphocyte antigen/B-lymphocyte surface antigen	yp1229w	p10275	AR	Androgen receptor	
ymr309c	q05682	CALD1	Caldesmon/CDM	yp1229w	q10571	MN1	Probable tumor suppressor protein MN1	
ymr309c	q07283	THH	Trichohyalin	yp1229w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	
ymr309c	q15696	U2AF1-RS2	U2 small nuclear ribonucleoprotein auxiliary factor 35 KD subunit related/protein 2	yp1229w	p54253	SCA1	Ataxin-1/spinocerebellar ataxia type 1 protein	
ymr309c	p20309	CHRM3	Muscarinic acetylcholine receptor M3	yal016w	p30153	PPP2R1A	Protein phosphatase PPP2A, 65kd regulatory subunit alpha-isotype	
ymr309c	ymr127w	p20309	CHRM3	Muscarinic acetylcholine receptor M3	ykr055w	p21181	CDC42	G25K GTP-binding protein
ymr309c	p48729	CSNK1A1	Casein kinase I, alpha isoform/CK1-alpha/CK1	ycd054w	q05682	CALD1	Caldesmon/CDM	
ymr309c	p48730	CSNK1D	Casein kinase I delta isoform	ycd054w	p35663	CYLC1	Cyclin I	
ymr309c	p49674	CSNK1E	Casein kinase I epsilon	ycd054w	p12883	MYH7	MYOSIN, CARDIAC, HEAVY CHAIN, BETA	
ymr309c	p51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	ycd054w	p19338	NCL	Nucleolin/protein C23	
ymr309c	p78368	CSNK1G2	Casein kinase I, gamma 2 isoform	ycd034w	p35579	MYH9	Myosin heavy chain, nonmuscle type A/cellular myosin heavy chain, type A/NMMHC-A	

<i>ym1154c</i>	p48730	CSNK1D	Casein kinase I delta isoform	<i>ym011c</i>	p45844	ABCG1	White protein homolog
<i>ym1154c</i>	p48729	CSNK1A1	Casein kinase I, alpha isoform/CK1-alpha/CK1	<i>yk204w</i>	p10163	PRB4	PROLINE-RICH PROTEIN, BISINI SUBFAMILY, 4
<i>ym1154c</i>	p48730	CSNK1D	Casein kinase I delta isoform	<i>yk204w</i>	p48634	BAT2	Large proline-rich protein BAT2/HLA-B-associated transcript 2
<i>ym1154c</i>	p49674	CSNK1E	Casein kinase I epsilon	<i>yk204w</i>	p54259	DRPLA	Atrophin-1/dentatorubral-pallidoluysian atrophy protein
<i>ym1154c</i>	p51812	RPS6KA3	Ribosomal protein S6 kinase II alpha 3/insulin-stimulated protein kinase 1	<i>yk204w</i>	p04280	PRB1	Salivary proline-rich protein/clone CP3, CP4, and CP5
<i>ym1154c</i>	p78368	CSNK1G2	Casein kinase I, gamma 2 isoform	<i>yk204w</i>	p02812	PRB2	Salivary proline-rich protein/Clone CP7
<i>ym1154c</i>	p48730	CSNK1D	Casein kinase I delta isoform	<i>ym267w</i>	q15181	PP	Inorganic pyrophosphatase [fragment]/PPase
<i>ym1154c</i>	p48730	CSNK1D	Casein kinase I delta isoform	<i>yor355w</i>	p42568	MLLT3	AF-9 protein
<i>ym1154c</i>	p49674	CSNK1E	Casein kinase I epsilon	<i>yor355w</i>	q14669	TRIP12	Thyroid receptor interacting protein 12/KIAA0045
<i>ym1189w</i>	p35222	CTNNB1	Beta-catenin.	<i>yr252w</i>	p33316	DUT	Deoxyuridine triphosphatase nucleotidohydrolyase
<i>ym1189w</i>	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	<i>yr252w</i>	p10265	PRT	Retrovirus-related protease
<i>ym1189w</i>	000505	KPNA3	Karyopherin alpha 3	<i>yhl009c</i>	p17861	XBP1	X box binding protein-1/XBP-1
<i>ym1189w</i>	000629	QIP1	Karyopherin alpha 4/Qip1	<i>yhl009c</i>	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein
<i>ym1189w</i>	p35222	CTNNB1	Beta-catenin.	<i>yhl009c</i>	p25054	APC	Adenomatous polyposis coli protein
<i>ym1189w</i>	p52292	KPNA2	Importin alpha-2 subunit/SRP1-alpha	<i>yhl009c</i>	p12270	TPR	Nucleoprotein TPR
<i>ym1189w</i>	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	<i>yhl009c</i>	q02224	CENPE	Centromeric protein E/CENP-E protein
<i>ym1189w</i>	p35222	CTNNB1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	<i>ylf159w</i>	p11766	ADH5	Class III alcohol dehydrogenase chi subunit
<i>ym1189w</i>	p52294	KPNA1	Beta-catenin.	<i>ylf159w</i>	q00796	SORD	Sorbitol dehydrogenase/L-iditol-2 dehydrogenase
<i>ym1189w</i>	p35222	CTNNB1	Beta-catenin.	<i>ylf303w</i>	p32929	CTH	Cystathione gamma-lyase
<i>ym1189w</i>	000505	KPNA3	Karyopherin alpha 3	<i>ymr028w</i>	p32119	TDPX1	Thioredoxin peroxidase 1/thioredoxin-dependent peroxide reductase 1/thiol-specific antioxidant protein/TSA/PRP/natural killer cell enhancing factor BINKEF-B
<i>ym1189w</i>	000629	QIP1	Karyopherin alpha 4/Qip1	<i>ymr028w</i>	q13162	AOE372	Thioredoxin peroxidase AOE372/antioxidant enzyme AOE372
<i>ym1189w</i>	p35222	CTNNB1	Beta-catenin.	<i>ymr028w</i>	q06830	TDPX2	Thioredoxin peroxidase 2/proliferation-associated gene (pag).
<i>ym1189w</i>	p52292	KPNA2	Importin alpha-2 subunit/SRP1-alpha	<i>ymr028w</i>	p30041	AOP2	Antioxidant protein 2
<i>ym1189w</i>	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	<i>ymr028w</i>	p30048	AOP1	Mitochondrial thioredoxin-dependent peroxide reductase/antioxidant protein 1
<i>ym1189w</i>	000505	KPNA3	Karyopherin alpha 3	<i>ymr226c</i>	p15428	PGDH1	15-Hydroxyprostaglandin dehydrogenase [NAD(+)]/PGDH
<i>ym1189w</i>	p35222	CTTNB1	Beta-catenin.	<i>ymr226c</i>	q02338	BDH	D-beta-hydroxybutyrate dehydrogenase
<i>ym1189w</i>	p52292	KPNA2	Importin alpha-2 subunit/SRP1-alpha	<i>ymr226c</i>	q92781	RDH1	11-cis retinol dehydrogenase
<i>ym1189w</i>	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	<i>ymr226c</i>	p14061	E2DH	Estradiol 17 beta-dehydrogenase
<i>ym1189w</i>	p35222	CTTNB1	Beta-catenin.	<i>yoj058w</i>	p00966	ASS	Argininosuccinate synthase/citrulline-aspartate ligase
<i>ym1189w</i>	p35222	CTTNB1	Beta-catenin.	<i>yp111w</i>	p78540	ARG2	Arginase 1/non-hepatic

ynl189w	p52294	KPNA1	Importin alpha-1 subunit/SRP1-beta/nucleoprotein interactor 1	ylp111w	p05089	ARG1	Arginase 1	
ynl210w	q00341	HBP	High density lipoprotein binding protein	ylk142w	p07942	LAMB1	Laminin beta-1 chain/laminin B1 chain	
ynl218w	p35249	RFC4	Activator 1 37 kD subunit/replication factor C, 37-kDa subunit	yf423c	p49454	CENPF	CENPF kinase/protein	
ynl218w	p35250	RFC2	Activator 1 40 kD subunit/replication factor C, 40 kDa subunit	yf423c	p15924	DSP	Desmoplakin I and II	
ynl218w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit	yf423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	
ynl218w	p40937	RFC5	Activator 1 36 kD subunit/replication factor C, 36-kDa subunit	yf423c	q02224	CENPE	Centromeric protein E/CENP-E protein	
ynl218w	p35249	RFC4	Activator 1 37 kD subunit/replication factor C, 37-kDa subunit	yl1218w	p35249	RFC4	Activator 1 37 kD subunit/replication factor C, 37-kDa subunit	
ynl218w	p35250	RFC2	Activator 1 40 kD subunit/replication factor C, 40 kDa subunit	yl1218w	p35250	RFC2	Activator 1 40 kD subunit/replication factor C, 40 kDa subunit	
ynl218w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit	yl1218w	p35251	RFC1	Replication factor C large subunit/activator 1140 Kd subunit	
ynl218w	p40937	RFC5	Activator 1 36 kD subunit/replication factor C, 36-kDa subunit	yl1218w	p40937	RFC5	Activator 1 36 kD subunit/replication factor C, 36-kDa subunit	
ynl287w	p21851	CLAPB1	Beta adaptin	ybr281c	p31146	CORO1	Coronin-like Protein P57	
ynl287w	q10567	ADTB1	Beta-adaptin 1	ybr281c	p35606	COPP	Beta subunit of coatomer complex	
ynl006w	p12036	NEFH	Neurofilament triplet H protein/200 kD neurofilament protein	yho022w	q15811	ITSN	Intersectin/SH3 domain-containing protein SH3P17	
68	ym006w	p26358	DNMT	DNA/cytosine-50methyl transferase/DNA methyltransferase/DNA metase/MCM7/M. HSAI	yho022w	q14247	CTTN	SRC substrate contactin/amplaxin
-	ym006w	p46100	ATRX	Transcriptional regulator ATRX/X-linked helicase II/X-linked nuclear protein	yho022w	p19174	PLCG1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma 1/phospholipase C-gamma 1
ym006w	p80303	NEFA	DNA binding protein NEFA	yhi002w	p163333	NCK	Cytoplasmic protein NCK	
ym006w	p98174	FGD1	Putative RHO/RAC guanine nucleotide exchange factor/facigennial dysplasia protein	yhi002w	p14317	HCLS1	Hematopoietic lineage cell specific protein	
ym006w	q02224	CENPE	Centromeric protein E/CENP-E protein	yhi002w	p29354	GRB2	Growth factor receptor-bound protein 2	
ym006w	q07283	THH	Trichohyalin	yhi002w	p98171	RGC1	RHO-GAP hematopoietic protein C1	
ym006w	q13438	OS9	Protein OS-9 precursor	yhi002w	p46109	CRKL	Crk-like protein	
ym006w	q92794	MOZ	Monocytic leukemia zinc finger protein	yhi002w	q13813	SPTA2	Spectrin alpha chain, brain/nonerythroid alpha-spectrin	
ym034w	p11055	MYH3	Embryonic myosin heavy chain.	Ymr117c	p04264	KRT1	Keratin, type II cytoskeletal 1/cytokeratin/hair alpha protein	
ym034w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	Ymr117c	p30622	RSN	Restin	
ym034w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	Ymr117c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/N/M/H-C-B	
ym034w	p15924	DSP	Desmoplakin I and II	Ymr117c	p11055	MYH3	Embryonic myosin heavy chain.	
ym034w	p49454	CENPF	CENPF kinase/protein	Ymr117c	p42566	EPS15	Epidermal growth factor receptor substrate 15	
ym034w	q02224	CENPE	Centromeric protein E/CENP-E protein	Ymr117c	p49454	CENPF	CENPF kinase/protein	
ym059w	p21695	GPDI	L-glycerol-3-phosphate dehydrogenase [NAD+]	yf017c	p08578	SNRPE	Small nuclear ribonucleoprotein E/snRNP-E	

yol061w	p09329	PRPS1	Phosphoribosyl pyrophosphate synthetase I/ribose-phosphate pyrophosphokinase I	yer09c	p09329	PRPS1	Phosphoribosyl pyrophosphate synthetase I/ribose-phosphate pyrophosphokinase I	
yol061w	p11908	PRPS2	Phosphoribosyl pyrophosphate synthetase subunit II	yer09c	p11908	PRPS2	Phosphoribosyl pyrophosphate synthetase subunit II	
yol061w	p21108	PRPS3	Phosphoribosyl pyrophosphate synthetase subunit III	yer09c	p21108	PRPS3	Phosphoribosyl pyrophosphate synthetase subunit III	
yol059w	p15924	DSP	Desmoplakin I and II	yer09c	p21108	PRPS3	Phosphoribosyl pyrophosphate synthetase subunit III	
yol059w	p49454	CENPF	CENP-F kinetochore protein	yer09c	p11908	PRPS2	Phosphoribosyl pyrophosphate synthetase subunit II	
yol059w	q02224	CENPE	Centromeric protein E/CENP-E protein	yer09c	p09329	PRPS1	PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE I	
yol059w	p12270	TPR	Nucleoprotein TPR	yfr423c	p05737	KRT8	Keratin, type II cytoskeletal 8/cyokeratin 8/K8/CK8	
yol059w	p12883	MYH7	Myosin heavy chain, cardiac muscle isoform	yfr423c	p30622	RSN	Reslin	
yol059w	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yfr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	
yol059w	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	yfr423c	q15431	SYCP1	Synaptonemal complex protein 1/SCP-1 protein	
yol059w	p15924	DSP	Desmoplakin I and II	yfr423c	p15924	DSP	Desmoplakin I and II	
yol059w	p30622	RSN	Reslin	yfr423c	p11047	LMC1	Laminin gamma-1 chain [precursor]/laminin B2 chain	
yol059w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yfr423c	p12270	TPR	Nucleoprotein TPR	
yol059w	p49454	CENPF	CENP-F kinetochore protein	yfr423c	p49454	CENPF	CENP-F kinetochore protein	
yol059w	q02224	CENPE	Centromeric protein E/CENP-E protein	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein	
yol059w	p13667	ERP72	Protein disulfide isomerase related protein/ERP72	yhr091c	p54136	RARS	ArgRS/glyiny-tRNA synthetase	
yol105c	q02505	MUC3	Mucin 3 [fragments]/intestinal mucin 3	ygi153w	q02224	CENPE	Centromeric protein E/CENP-E protein	
yol105c	q99102	MUC4	Tracheo-bronchial mucin 4/mucin 4 [fragment]	ygi153w	q03001	BPAF1	Bullous 230 kDa periphigoid antigen 1	
-	yol108c	p98171	RGC1	RHO-GAP hematopoietic protein C1	yki135c	p38935	IGHMBP2	DNA-binding protein SMBP2
yol108c	p98171	RGC1	RHO-GAP hematopoietic protein C1	yki135c	q10567	ADTB1	Beta-adaptin 1	
yol108c	p98171	RGC1	RHO-GAP hematopoietic protein C1	yml317w	q02817	MUC2	Intestinal mucin 2/mucin 2	
yol111c	p11441	GDX	Ubiquitin-like protein GDY	yor007c	p50502	HIP	Progesterone receptor-associated p48 protein	
yol111c	p54725	RAD23A	UV excision repair protein RAD23 homolog	yor007c	p30260	CDC27	Protein CDC27HS/cell division cycle protein 27	
yol111c	p54727	D21090	A/HHR23A UV excision repair protein RAD23 homolog B/XPC repair complementing protein (p58/HFR23B), complete cds.	yor007c	q08752	PPID	40 kD peptidyl-prolyl CIS-TRANS isomerase/cyclophilin-40 mRNA, complete cds.	
yol123w	p07029	UP2	Helogenous nuclear ribonucleoprotein UP2	ygl122c	p20226	TBP	TATA-binding protein/transcription initiation factor TFIID	
yol123w	p09651	HNRPA1	Helogenous nuclear ribonucleoprotein A1/heixin-stabilizing protein/single-strand binding protein/HNRNP core protein A1	ygl122c	q10571	MN1	Probable tumor suppressor protein MN1	
yol123w	p11940	PABPL1	PolyA binding protein 1	ygl122c	q14814	MEF2D	Myocyte-specific enhancer factor 2D	
yol123w	p22626	HNRPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	ygl122c	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	
yol123w	p26378	ELAVL4	Paraneoplastic encephalomyelitis antigen 3	ygl122c	p42858	HD	Huntingtin/huntington's disease protein	
yol123w	p38159	HNRPG	Heterogeneous nuclear ribonucleoprotein G/HNRP G/glycoprotein P43	ygl122c	q92794	MOZ	Monocytic leukemia zinc finger protein	
yol123w	q15427	SAP49	Spliceosome associated protein 49/SAP49	ygl122c	q93074	KIAA0192	Hypothetical protein KIAA0192	
yol130w	p46821	MAP1B	Microtubule-associated protein 1B	ygl025c	q02078	MEF2A	Mycocyte-specific enhancer factor 2A	
yol130w	q04724	TLE1	Transducin-like enhancer protein	ygl025c	q02817	MUC2	Intestinal mucin 2/mucin 2	
yol130w	p46821	MAP1B	Microtubule-associated protein 1B	yfr291c	q14232	ELF2B1	Translation initiation factor eIF-2B alpha subunit	
yol130w	q04724	TLE1	Transducin-like enhancer protein	yfr291c	p49770	EIF2B2	Translation initiation factor EIF-2B beta subunit/S20lii/15	

yor061w	p24941	CDK2	Cell division protein kinase 2	yor039w	p13862	CSNK2B
yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and ycr057c	p35226	BMI1	DNA-binding protein BMI1
yor128c	p22234	PAICS	AIR carboxylase of the purine pathway			AF-9 protein
yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and ycr057c	p42568	MLLT3	ADE2 showing homologies to SAICAR synthetase and AIR carboxylase of the purine pathway
yor128c	p22234	PAICS	AIR carboxylase of the purine pathway	p22234	PAICS	AIR carboxylase of the purine pathway
yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and yor128c			Neuronal kinesin heavy chain
yor128c	p22234	PAICS	AIR carboxylase of the purine pathway			CENP-F kinetochore protein
yor128c	p22234	PAICS	ADE2 showing homologies to SAICAR synthetase and yor128c			Centromeric protein E/CENP-E protein
yor128c	p22234	PAICS	AIR carboxylase of the purine pathway			Myosin heavy chain, cardiac muscle alpha isoform
yor132w	q00839	HNRNPU	Heterogenous nuclear ribonucleoprotein U/scaffold	yor069w	q12840	KIF5C
yor269w	p25398	GNB2-RS1	Guanine nucleotide-binding protein beta subunit-like	yor254c	p49454	CENPF
yor269w	p35606	COPP	Guanine nucleotide-binding protein beta subunit-like	yor254c	q02224	CENPE
yor269w	p43034	PAFAH1B1	Beta subunit of coatomer complex	yor254c	p13533	MYH6
yor303w	p31327	CPS1	Platelet activating factor acetylhydrolase 1B alpha subunit	yor039w	p13862	CSNK2B
yor348c	p52569	SLC7A2	Carbamoyl-phosphate synthase [ammonia], mitochondrial [precursor]	yor039w	p29144	TTP2
yor348c	p52569	SLC7A2	Low-affinity cationic amino acid transporter-2/CAT-2	ycf045c	q03164	Zinc finger protein HRX
yor348c	p52569	SLC7A2	Low-affinity cationic amino acid transporter-2/CAT-2	yjl084c	q01082	Beta-spectrin chain, brain
yor348c	p52569	SLC7A2	Low-affinity cationic amino acid transporter-2/CAT-2	Ymr238w	p49454	CENP-F kinetochore protein
yor353c	p22792	CPN2	Carboxypeptidase N	ygr120c	p49454	Apollipoprotein B
yor353c	p22792	Cpn2	IGF binding protein complex acid-labile	ygr120c	p04114	Resin
yor353c	p35858	IGFALS	Fibromodulin	ygr120c	p30622	Serine/threonine-protein kinase PAK-gamma
yor353c	p06828	FMOD	Bone proteoglycan II [precursor]/FG40	yhr102w	q13177	PAK2
yor353c	p07585	DCN	Carboxypeptidase N	yhr102w	q02750	Dual specificity mitogen-activated protein kinase kinase 1
yor353c	p22792	Cpn2	Oligodendrocyte-myelin glycoprotein	yhr102w	q13153	Serine/threonine-protein kinase PAK-alpha
yor353c	p23515	OMG	IGF binding protein complex acid-labile	yhr102w	q99759	Mitogen-activated protein kinase kinase kinase 3
yor353c	p35858	IGFALS	Fibromodulin	yhr102w	MAP2K3	Dual specificity mitogen-activated protein kinase kinase kinase 3
-	-	-	Garp protein/Garpin	yhr102w	MAP2K4	Dual specificity mitogen-activated protein kinase kinase kinase 4
yor353c	q06628	FMOD	Tracheo-bronchial mucin 4/mucin 4 [fragment]	yhr102w	q13163	MAP2K5
yor353c	q14392	GARP	Prosome subunit C2.	yhr102w	p51955	Serine/threonine-protein kinase NEK2
yor353c	q99102	MUC4	Glutamate dehydrogenase 1	yfl017c	p08578	Small nuclear ribonucleoprotein EsnRNP-E
yor362c	p25786	PSMA1	Glutamate dehydrogenase 2	yjl124c	p14678	Small nuclear ribonucleoprotein associated proteins B and B'
yor375c	p00367	GLUD1	AF-4 protein	yjl124c	p14648	Small nuclear ribonucleoprotein associated protein N
yor375c	p49448	GLUD2	Glutamate dehydrogenase 2	ydr480w	LGAL53	Galectin-3/IgE-binding protein
yp049c	p51825	MLLT2	Glutaredoxin	p17931	TBP	TATA-binding protein/transcription initiation factor TFIID
yp059w	p35754	GLRX	Glutaredoxin.	p20226	q99418	ARF nucleotides-binding site opener/ARNO protein/ARF exchange factor
yp059w	p35754	GLRX		ARNO		Mitogen-activated protein kinase 11
yp140c	p45985	MAP2K4	Dual specificity mitogen-activated protein kinase kinase 4	yhr030c	q15759	MAPK11

yp1140c	p46734	MAP2K3	Dual specificity mitogen-activated protein kinase kinase 3/MAP kinase kinase 3	yhr030c	p53778	MAPK12	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6
yp1140c	p52564	MAP2K6	Dual specificity mitogen-activated protein kinase kinase 6	yhr030c	p27361	MAPK3	Mitogen-activated protein kinase 3/extracellular signal-regulated kinase 1
yp1140c	q02750	PRKMK1	Dual specificity mitogen-activated protein kinase kinase 1	yhr030c	q13164	MAPK7	Mitogen-activated protein kinase 7/ERK5
yp1140c	q13163	MAP2K5	Dual specificity mitogen-activated protein kinase kinase 5	yhr030c	q16539	MAPK14	Mitogen-activated protein kinase 14/CSBP
yp1140c	q99759	MAP3K3	Mitogen-activated protein kinase kinase kinase 3/MEK kinase 3	yhr030c	p28482	MAPK1	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2
yp1151c	p35606	COPP	Beta subunit of coatomer complex	yor036w	q02224	CENPE	Centromeric protein E/CENP-E protein
yp1151c	p43034	PAFAH1B1	Platelet-activating factor acetylhydrolase 1B alpha subunit	yor036w	p49454	CENPF	CENP-F kinetochore protein
yp1151c	q15542	TAF2D	Transcription initiation factor TFIID 100 Kd subunit/TAFII-100/TAFII100	yor036w	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B
yp1174c	p49454	CENPF	CENP-F kinetochore protein	yhr1129c	p42024	ACTR1A	Alpha-centracrin
yp1174c	q02224	CENPE	Centromeric protein E/CENP-E protein	yhr1129c	p42025	ACTR1B	Beta-centracrin
yp1174c	p11055	MYH3	Embryonic myosin heavy chain.	yil144w	p11055	MYH3	Embryonic myosin heavy chain.
yp1174c	p12882	MYSS	Myosin heavy chain skeletal muscle, light meromyosin region	yil144w	p30622	RSN	Restin
yp1174c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yil144w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform
yp1174c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yil144w	p13533	MYH6	Myosin heavy chain, nonmuscle type A/cellular myosin
yp1174c	p30622	RSN	Restin	yil144w	p35579	MYH9	Myosin heavy chain, type A/NMMHC-A
-	-	-	-	yil144w	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yp1174c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yil144w	p49454	CENPF	CENP-F kinetochore protein
yp1174c	p49454	CENPF	CENP-F kinetochore protein	yil144w	q02224	CENPE	Centromeric protein E/CENP-E protein
yp1174c	q02224	CENPE	Centromeric protein E/CENP-E protein	yil144w	p15924	DSP	Desmoplakin I and II
yp1174c	q14203	DCTN1	Dynactin, 150 KD isoform [fragment]	yil144w	p12270	TPR	Nucleoprotein TPR
yp1174c	p11055	MYH3	Embryonic myosin heavy chain.	yil423c	p11047	LAMC1	Laminin gamma-1 chain [precursor]/laminin B2 chain
yp1174c	p12882	MYSS	Myosin heavy chain skeletal muscle, light meromyosin region	yil423c	p30622	RSN	Restin
yp1174c	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform	yil423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle
yp1174c	p13533	MYH6	Myosin heavy chain, cardiac muscle alpha isoform	yil423c	p05787	KRT8	Keratin, type II cytoskeletal 8/cytokeratin B/K8/CK8
yp1174c	p30622	RSN	Restin	yil423c	q15431	SYCP1	Syntaptonemal complex protein 1/SCP-1 protein
yp1174c	p35580	MYH10	Myosin heavy chain, nonmuscle type B/cellular myosin heavy chain, type B/NMMHC-B	yil423c	p49454	CENPF	CENP-F kinetochore protein
yp1174c	p49454	CENPF	CENP-F kinetochore protein	yil423c	q02224	CENPE	Centromeric protein E/CENP-E protein
yp1174c	q02224	CENPE	Centromeric protein E/CENP-E protein	yil423c	p15924	DSP	Desmoplakin I and II
yp1174c	q14203	DCTN1	Dynactin, 150 KD isoform [fragment]	yk135c	q10567	ADTB1	Beta-adaplin 1
yp1259c	p53677	P47B	Clathrin coat assembly protein AP47 homolog 2	yk135c	p21851	CLAPB1	Beta adaptin
yp1259c	p53580	CLAPS2	Clathrin coat assembly protein AP17/clathrin coat associated protein AP17	yil144w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform
yp1260w	p12270	TPR	Nucleoprotein TPR	yil144w	p12883	MYH7	Myosin heavy chain, cardiac muscle beta isoform

yp1260w	p17661	DES	Desmin	yil144w	p30622	RSN
yp1260w	p33176	KNS1	Kinesin heavy chain	yil144w	DSP	Desmoplakin I and II
yp1260w	p49454	CENPF	CENPF	yil144w	p15924	CENPF
yp1260w	q02224	CENPE	Centromeric protein E/CENPF-E protein	yil144w	p49454	CENPF
yp1260w	q15032	KIAA0029	Centromeric protein KIAA0029	yil144w	q02224	CENPE
yp1260w	q15431	SYCP1	Hypothetical protein 1/SYCP-1 protein	yil144w	p13535	MYH8
yp1260w	q16787	LAMA3	Synaptonemal complex protein 1/SYCP-1 protein	yil144w	p11055	MYH3
yp1260w	p35241	RDX	Laminin alpha-3 chain	yil144w	p13533	MYH6
yp1260w	p35580	MYH10	Radixin	yil144w	q00628	PTSR
yp018w	p46821	MAP1B	Myosin heavy chain, nonmuscle type B/cellular	ybr195c	p04901	GNB1
yp018w	q02832	BLSA	myosin heavy chain, type B/NMMHC-B	ybr195c	q09028	RBAP48
yp018w	q14203	DCTN1	Microtubule-associated protein 1B	ybr195c	q11016	GNB2
yp018w	q16643	DBN1	B-lymphocyte antigen/B-lymphocyte surface antigen	ybr195c	q16576	RBBP7
yp018w	p29475	NOS1	Dynactin, 150 kD isoform [fragment]	ybr195c	p16520	GNB3
yp048w	p35228	NOS2	Nitric oxide synthase/neuronal NOS	yor355w	p42568	MLLT3
yp054w	p28482	MAPK1	Inducible nitric oxide synthase	yor355w	q14669	TRIP12
-	p53778	MAPK12	Mitogen-activated protein kinase 1/extracellular signal-regulated kinase 2	yf029c	p24941	CDK2
yp054w	p53779	MAPK10	Mitogen-activated protein kinase 12/ERK6/extracellular signal-regulated kinase 6	yf029c	p50613	CDK7
yp054w	q13164	MAPK7	Mitogen-activated protein kinase 10	yf029c	p49840	GSK3A
yp054w	q15759	MAPK11	Mitogen-activated protein kinase 7/ERK5	yf029c	q00536	CDK3
yp054w	q16539	MAPK14	Mitogen-activated protein kinase 11	yf029c	p49841	GSK3B
yp105c	p07197	NEFM	Mitogen-activated protein kinase 14/CSBP	yf029c	q00535	CDK5
yp105c	p07197	NEFM	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	ygl145w	p35749	MYH11
yp105c	p07197	NEFM	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	ygl153w	q03001	BPAG1
yp105c	p07197	NEFM	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	ygr120c	p04114	APOB
yp110c	p19387	POLR2C	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	yhr050w	p25799	PSMA4
yp110c	p19387	POLR2C	Neurofilament triplet M protein/160 kD neurofilament protein/NF-M	yil1238w	p49454	CENPF
yp110c	p19387	POLR2C	DNA-directed RNA polymerase II 33kDa subunit RPB33	yil113w	q06481	APLP2
yp110c	p19387	POLR2C	DNA-directed RNA polymerase II 33kDa subunit RPB33	ybr135w	p33561	CKS1
yp119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ybr135w	p10275	AR
yp119w	p20248	CCNA	G2/mitotic-specific cyclin A.	ybr135w	p36777	LONN
yp119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ydr412w	p36776	LONM
yp119w	p20248	CCNA	G2/mitotic-specific cyclin A.			

yr119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	yrh035w	q15437	SEC23B	Protein transprot protein Sec23 B isoform	
yr119w	p20248	CCNA	G2/mitotic-specific cyclin A.	yrh035w	q15436	SEC23A	Protein transprot protein Sec23 A isoform	
yr119w	p14635	CCNB1	G2/mitotic-specific cyclin B1	ynl135c	FKBP3	Rapamycin-selective 25 Kd immunophilin		
yr119w	p20248	CCNA	G2/mitotic-specific cyclin A.	ynl135c	FKBP2	FK506-binding protein/FKBP-13		
yr119w	q03527	PSMC1	26S protease (S4) regulatory subunit	yrh025w	p14314	PRKCSH	Protein kinase C substrate, 80 kD protein, heavy chain/80K-H protein	
yr173c	q13608	PEX6	Peroxisome assembly factor-2/peroxisomal-type ATPase 1	yrh025w	q14203	DCTN1	Dynactin, 150 kD Isoform [fragment]	
yr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIIID	ygr180w	p22694	PRKACB	Testis-specific cAMP-dependent protein kinase catalytic subunit C-beta Isoform	
yr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ygr180w	p17612	PRKACA	CAMP-dependent protein kinase catalytic subunit type alpha	
yr185w	p54252	MJD1	Machado-Joseph disease protein 1	ygr180w	p54646	PRKAA2	5'-AMP-activated protein kinase, catalytic alpha-2 chain	
yr185w	q10571	MN1	Probable tumor suppressor protein MN1	ygr180w	q04759	PRKCQ	Protein kinase C-theta type	
yr185w	q93074	KIAA0192	Hypothetical protein KIAA0192	ygr180w	p27448	P78	Putative serine/threonine-protein kinase P78	
yr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIIID	ygr120c	p30622	RSN	Restin	
yr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ygr120c	p49454	CENPF	CENPF-kinetochore protein	
yr185w	p54252	MJD1	Machado-Joseph disease protein 1	ygr120c	p04114	APOB	Apolipoprotein B	
yr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIIID	ygr253c	p25788	PSMA3	Proteasome subunit C8	
-	yr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	ygr253c	p25787	PSMA2	Proteasome subunit C3
73	yr185w	p54252	MJD1	Machado-Joseph disease protein 1	ygr253c	p25786	PSMA1	Proteasome subunit C2.
yr185w	q10571	MN1	Probable tumor suppressor protein MN1	ygr253c	p34062	PSMA6	Proteasome lola chain/PROS-27	
-	yr185w	q93074	KIAA0192	Hypothetical protein KIAA0192	ygr253c	p25789	PSMA4	Proteasome subunit C9
-	yr185w	p20226	TBP	TATA-binding protein/transcription initiation factor TFIIID	yfr423c	p15924	DSP	Desmoplakin I and II
yr185w	p51531	SMARCA2	Possible global transcription activator SNF2L2/BRM	yfr423c	p48454	CENPF	CENPF-kinetochore protein	
yr185w	p54252	MJD1	Machado-Joseph disease protein 1	yfr423c	q02224	CENPE	Centromeric protein E/CENP-E protein	
yr185w	q10571	MN1	Probable tumor suppressor protein MN1	yfr423c	p30622	RSN	Restin	
yr185w	q93074	KIAA0192	Hypothetical protein KIAA0192	yfr423c	p13535	MYH8	Myosin heavy chain, perinatal skeletal muscle	

The human polypeptides disclosed in Table 7 are related as orthologs to yeast polypeptides that interact to form complexes according to the invention. Table 7 reflects this relationship and specifies a yeast accession number for a given human ortholog. In particular, Table 7 includes in column 1 the yeast accession number for the yeast "bait" sequence corresponding to the indicated human ortholog. Columns 2-4 provide the accession number of the human ortholog, the name of the human ortholog, and a description of the human ortholog, respectively, of the yeast "bait sequence". Column 5 of Table 7 provides the yeast accession number of the yeast "prey" sequence. Columns 6-8 provide the accession number of the human ortholog, the name of the human ortholog, and a description of the human ortholog, respectively, of the yeast "prey sequence".

In certain embodiments, one of the ortholog polypeptides includes a "bait" polypeptide selected from the polypeptides recited in Table 7, column 2, and the other ortholog polypeptide includes a "prey" protein selected from the polypeptides recited in Table 7, column 6. The yeast orthologs of these proteins are set out in columns 1 and 4 of Table 7, respectively. In some embodiments the first and second polypeptides of the complex are the polypeptides enumerated in Table 7. In some embodiments a first polypeptide is a "bait" polypeptide and a second polypeptide is "target" polypeptide, while in other embodiments the first polypeptide is a "target" polypeptide and the second is a "bait" polypeptide. Conservative variants of either polypeptide which retain binding specificity are within the scope of the invention, as are labeled forms of the complexes, as described above.

In other embodiments, the polypeptides are the binding domains of the "bait" and "prey" polypeptides listed in Table 7. A binding domain of a given first polypeptide may be any number of amino acids sufficient to specifically bind to, and complex with, the corresponding second polypeptide under conditions suitable for complex formation. A binding domain may be the minimal number of amino acids required to retain binding affinity, or may be a larger fragment or derivative of the polypeptides listed in Table 7, columns 2 and 6.

In certain embodiments, the "bait" polypeptides of the ortholog complex are polypeptides categorized, for example, as a "Metabolism" protein in the MIPS database. In

some embodiments, the “prey” protein of the complex is also a “Metabolism” protein, while in other embodiments the “prey” protein is, for example, an “Unclassified” protein (*see* Table 7). Other exemplary MIPS categories include, *e.g.*, “Cell Growth/Cell Division/DNA Synthesis” proteins (*see* Table 2).

5 In a further aspect, the invention provides chimeric polypeptide complex that includes at least one yeast polypeptide and at least one human ortholog of the corresponding interacting yeast polypeptide. In one embodiment, there is provided a purified chimeric complex including a yeast “bait” polypeptide selected from the polypeptides recited in Table 7, column 1 and a human ortholog of the corresponding yeast “prey” polypeptide; the human ortholog is  
10 selected from the polypeptides recited in Table 7, column 6 (while the corresponding yeast “prey” proteins are recited in column 5). For example, with reference to Table 7, first row, in one embodiment, a chimeric protein containing YAL032C and P16118 is provided (P16118 is the human ortholog of corresponding yeast “prey” protein YLR345W).

In other embodiments, the complex contains a human ortholog of a yeast “bait”  
15 protein and a yeast “prey” protein. The yeast “prey” protein is selected from the polypeptides recited in Table 7, column 5, and the human ortholog of the corresponding yeast “bait” protein is selected from the polypeptides recited in Table 7, column 2 (while the corresponding yeast “bait” proteins themselves are recited in column 1). For example, with reference to Table 7, first row, in one embodiment, a chimeric protein containing Q13573 and YLR345W is  
20 provided (Q13573 is the human ortholog of corresponding yeast “bait” protein YAL032C).

In certain embodiments the first and second polypeptides of the chimeric complex are the polypeptides recited in Table 7, columns 1 and 6, or columns 2 and 5, respectively, while in other embodiments, the polypeptides of the chimeric complex contain the polypeptides recited in Table 7. Conservative variants of either polypeptide which retain binding specificity  
25 are within the scope of the invention, as are labeled forms of the chimeric complexes, and chimeric complexes of binding domains, as described above.

### Chimeric Polypeptides, DNA, Vectors and Recombinant Cells

In a further aspect, the invention provides a chimeric polypeptide that includes sequences of two interacting proteins according to the invention. The interacting proteins can  
30 be, *e.g.*, the interacting protein pairs disclosed in Tables 3-7, herein. Also included are chimeric polypeptides including multimers, *i.e.*, sequences from two or more pairs of interacting proteins. An example of such a chimeric polypeptide is a polypeptide that includes

amino acid sequences from ProPair1a and 1b, and from ProPair 2a and 2b. The chimeric polypeptide includes a region of a first protein covalently linked, e.g. via peptide bond, to a region of a second protein. In certain embodiments, the second protein is a species ortholog of the first protein. In some embodiments, the chimeric polypeptide contains regions of first and second proteins from yeast, where the proteins are selected from the "bait" and corresponding "prey" proteins recited in Table 3, columns 1 and 4, respectively. In other embodiments, the chimeric polypeptide contains regions of first and second human ortholog proteins, where the proteins are selected from the "bait" and corresponding "prey" proteins recited in Table 7, columns 2 and 6, respectively (the yeast orthologs of these proteins are recited in columns 1 and 5, respectively). In still other embodiments, the chimeric polypeptide contains regions of a first protein from yeast, and a second human ortholog protein, where the yeast proteins are selected from the "bait" and corresponding "prey" proteins recited in Table 7, columns 1 and 5, respectively, while the human ortholog proteins are selected from the "bait" and corresponding "prey" proteins recited in Table 7, columns 2 and 6, respectively.

In some embodiments, the chimeric polypeptide(s) of the complex include(s) six or more amino acids of a first protein covalently linked to six or more amino acids of a second protein. In other embodiments, the chimeric polypeptide includes at least one binding domain of a first or second protein.

Preferably, the chimeric polypeptide includes a region of amino acids of the first polypeptide able to bind to a second polypeptide. Alternatively, or in addition, the chimeric polypeptide includes a region of amino acids of the second polypeptide able to bind to the first polypeptide.

Nucleic acid encoding the chimeric polypeptide, as well as vectors and cells containing these nucleic acids, are within the scope of the present invention. The chimeric polypeptides can be constructed by expressing nucleic acids encoding chimeric polypeptides using recombinant methods, described above, then recovering the chimeric polypeptides, or by chemically synthesizing the chimeric polypeptides. Host-vector systems that can be used to express chimeric polypeptides include, e.g.: (i) mammalian cell systems which are infected with vaccinia virus, adenovirus; (ii) insect cell systems infected with baculovirus; (iii) yeast containing yeast vectors or (iv) bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. Depending upon the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

The expression of the specific proteins may be controlled by any promoter/enhancer known in the art including, e.g.: (i) the SV40 early promoter (see e.g., Bernoist & Chambon, *Nature* 290: 304-310 (1981)); (ii) the promoter contained within the 3'-terminus long terminal repeat of Rous Sarcoma Virus (see e.g., Yamamoto, *et al.*, *Cell* 22: 787-797 (1980)); (iii) the Herpesvirus thymidine kinase promoter (see e.g., Wagner, *et al.*, *Proc. Natl. Acad. Sci. USA* 78: 1441-1445 (1981)); (iv) the regulatory sequences of the metallothionein gene (see e.g., Brinster, *et al.*, *Nature* 296: 39-42 (1982)); (v) prokaryotic expression vectors such as the  $\beta$ -lactamase promoter (see e.g., Villa-Kamaroff, *et al.*, *Proc. Natl. Acad. Sci. USA* 75: 3727-3731 (1978)); (vi) the *tac* promoter (see e.g., DeBoer, *et al.*, *Proc. Natl. Acad. Sci. USA* 80: 21-25 (1983)).

Plant promoter/enhancer sequences within plant expression vectors may also be utilized including, e.g.: (i) the nopaline synthetase promoter (see e.g., Herrar-Estrella, *et al.*, *Nature* 303: 209-213 (1984)); (ii) the cauliflower mosaic virus 35S RNA promoter (see e.g., Garder, *et al.*, *Nuc. Acids Res.* 9: 2871 (1981)) and (iii) the promoter of the photosynthetic enzyme ribulose bisphosphate carboxylase (see e.g., Herrera-Estrella, *et al.*, *Nature* 310: 115-120 (1984)).

Promoter/enhancer elements from yeast and other fungi (e.g., the Gal4 promoter, the alcohol dehydrogenase promoter, the phosphoglycerol kinase promoter, the alkaline phosphatase promoter), as well as the following animal transcriptional control regions, which possess tissue specificity and have been used in transgenic animals, may be utilized in the production of proteins of the present invention.

Other animal transcriptional control sequences derived from animals include, e.g.: (i) the insulin gene control region active within pancreatic  $\beta$ -cells (see e.g., Hanahan, *et al.*, *Nature* 315: 115-122 (1985)); (ii) the immunoglobulin gene control region active within lymphoid cells (see e.g., Grosschedl, *et al.*, *Cell* 38: 647-658 (1984)); (iii) the albumin gene control region active within liver (see e.g., Pinckert, *et al.*, *Genes and Devel.* 1: 268-276 (1987)); (iv) the myelin basic protein gene control region active within brain oligodendrocyte cells (see e.g., Readhead, *et al.*, *Cell* 48: 703-712 (1987)); and (v) the gonadotrophin-releasing hormone gene control region active within the hypothalamus (see e.g., Mason, *et al.*, *Science* 234: 1372-1378 (1986)).

The vector may include a promoter operably-linked to nucleic acid sequences which encode a chimeric polypeptide, one or more origins of replication, and optionally, one or more selectable markers (e.g., an antibiotic resistance gene). A host cell strain may be selected

which modulates the expression of chimeric sequences, or modifies/processes the expressed proteins in a desired manner. Moreover, different host cells possess characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation, and the like) of expressed proteins. Appropriate cell lines or  
5 host systems may thus be chosen to ensure the desired modification and processing of the foreign protein is achieved. For example, protein expression within a bacterial system can be used to produce an unglycosylated core protein; whereas expression within mammalian cells ensures "native" glycosylation of a heterologous protein.

### Antibodies Specific for Polypeptide Complexes

10 The invention further provides antibodies and antibody fragments (such as Fab or (Fab)<sub>2</sub> fragments) that bind specifically to the complexes described herein. By "specifically binds" is meant an antibody that recognizes and binds to a particular polypeptide complex of the invention, but which does not substantially recognize or bind to other molecules in a sample, or to any of the polypeptides of the complex when those polypeptides are not  
15 complexed.

For example, a purified complex, or a portion, variant, or fragment thereof, can be used as an immunogen to generate antibodies that specifically bind the complex using standard techniques for polyclonal and monoclonal antibody preparation.

20 A full-length polypeptide complex can be used, if desired. Alternatively, the invention provides antigenic fragments of polypeptide complexes for use as immunogens. In some embodiments, the antigenic complex fragment includes at least 6, 8, 10, 15, 20, or 30 or more amino acid residues of a polypeptide. In one embodiment, epitopes encompassed by the antigenic peptide include the binding domains of the polypeptides, or are located on the surface of the protein, e.g., hydrophilic regions.

25 If desired, peptides containing antigenic regions can be selected using hydropathy plots showing regions of hydrophilicity and hydrophobicity. These plots may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, *Proc. Nat. Acad. Sci. USA* 78:3824-3828 (1981); Kyte and Doolittle, *J. Mol. Biol.* 157:105-142  
30 (1982).

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as a polypeptide complex. Such antibodies include, *e.g.*, polyclonal, monoclonal, chimeric, single chain, Fab and F(ab')<sub>2</sub> fragments, and an Fab expression library. In specific embodiments, 5 antibodies to human ortholog complexes.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies. For example, for the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by 10 injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polypeptide complex. Alternatively, the immunogenic polypeptides or complex may be chemically synthesized, as discussed above. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, *e.g.*, Freund's 15 (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lyssolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against complex can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known 20 techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide complex. A monoclonal antibody composition thus typically displays a single binding affinity for a 25 particular protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular complex, or polypeptide, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, *e.g.*, the hybridoma technique (*see* Kohler & Milstein, *Nature* 256: 495-497 (1975)); the trioma technique; the human B-cell hybridoma technique (*see* Kozbor, *et al.*, *Immunol Today* 4: 72 (1983)); and the EBV hybridoma technique to produce human 30 monoclonal antibodies (*see* Cole, *et al.*, In: *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., (1985) pp. 77-96). If desired, human monoclonal antibodies may be prepared by using human hybridomas (*see* Cote, *et al.*, *Proc. Natl. Acad. Sci. USA* 80: 2026-2030 (1983))

or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, In: *Monoclonal Antibodies and Cancer Therapy, supra*).

Methods can be adapted for the construction of F<sub>ab</sub> expression libraries (see e.g., Huse, *et al.*, *Science* 246: 1275-1281 (1989)) to allow rapid and effective identification of

- 5 monoclonal F<sub>ab</sub> fragments with the desired specificity for the desired protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See e.g., U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polypeptide or polypeptide complex may be produced by techniques known in the art including, e.g.: (i) an F<sub>(ab')2</sub> fragment produced by pepsin digestion  
10 of an antibody molecule; (ii) an F<sub>ab</sub> fragment generated by reducing the disulfide bridges of an F<sub>(ab')2</sub> fragment; (iii) an F<sub>ab</sub> fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F<sub>v</sub> fragments.

Chimeric and humanized monoclonal antibodies against the polypeptide complexes, or polypeptides, described herein are also within the scope of the invention, and can be produced  
15 by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.*, *Science* 240: 1041-1043 (1988); Liu *et al.*, *Proc.  
20 Nat. Acad. Sci. USA* 84: 3439-3443 (1987); Liu *et al.*, *J. Immunol.* 139: 3521-3526 (1987); Sun *et al.*, *Proc. Nat. Acad. Sci. USA* 84: 214-218 (1987); Nishimura *et al.*, *Cancer Res.* 47: 999-1005 (1987); Wood *et al.*, *Nature* 314: 446-449 (1985); Shaw *et al.*, *J. Natl. Cancer Inst.* 80: 1553-1559 (1988); Morrison, *Science* 229: 1202-1207 (1985); Oi *et al.*, *BioTechniques* 4: 214 (1986); U.S. Pat. No. 5,225,539; Jones *et al.*, *Nature* 321: 552-525 (1986); Verhoeven *et  
25 al.*, *Science* 239: 1534 (1988); and Beidler *et al.*, *J. Immunol.* 141: 4053-4060 (1988).

Methods for the screening of antibodies that possess the desired specificity include, e.g., enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. For example, selection of antibodies that are specific to a particular domain of a polypeptide complex is facilitated by generation of hybridomas that  
30 bind to the complex, or fragment thereof, possessing such a domain.

In certain embodiments of the invention, antibodies specific for the polypeptide complexes described herein may be used in various methods, such as detection of complex, and identification of agents which disrupt complexes. These methods are described in more

detail, below. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

Polypeptide complex-specific, or polypeptide-specific antibodies, can also be used to isolate complexes using standard techniques, such as affinity chromatography or immunoprecipitation. Thus, the antibodies disclosed herein can facilitate the purification of specific polypeptide complexes from cells, as well as recombinantly produced complexes expressed in host cells.

### Kits

In a specific embodiment, the invention provides kits containing a reagent, for example, an antibody described above, which can specifically detect a polypeptide complex, or a constituent polypeptide, described herein. Such kits can contain, for example, reaction vessels, reagents for detecting complex in sample, and reagents for development of detected complex, *e.g.* a secondary antibody coupled to a detectable marker. The label incorporated into the anti- complex, or anti-polypeptide antibody may include, *e.g.*, a chemiluminescent, enzymatic, fluorescent, colorimetric or radioactive moiety. Kits of the present invention may be employed in diagnostic and/or clinical screening assays.

### Pharmaceutical Compositions

The invention further provides pharmaceutical compositions of purified complexes suitable for administration to a subject, most preferably, a human, in the treatment of disorders involving altered levels of such complexes. Such preparations include a therapeutically-effective amount of a complex, and a pharmaceutically acceptable carrier. As utilized herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal

or a state government or listed in the U.S. Pharmacopoeia or other generally recognized pharmacopoeia for use in animals and, more particularly, in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered and includes, but is not limited to such sterile liquids as water and oils.

5       The therapeutic amount of a complex which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and may be determined by standard clinical techniques by those of average skill within the art. In addition, *in vitro* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of  
10 administration, and the overall seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. // However, suitable dosage ranges for intravenous administration of the complexes of the present invention are generally about 20-500 micrograms ( $\mu\text{g}$ ) of active compound per kilogram (Kg) body weight. Suitable dosage ranges for intranasal administration are generally about 0.01  
15 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems. Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

Various delivery systems are known and can be used to administer a pharmaceutical  
20 preparation of a complex of the invention including, e.g.: (i) encapsulation in liposomes, microparticles, microcapsules; (ii) recombinant cells capable of expressing the polypeptides of the complex; (iii) receptor-mediated endocytosis (see, e.g., Wu *et al.*, *J. Biol. Chem.* 262: 4429-4432 (1987)); (iv) construction of a nucleic acid encoding the polypeptides of the complex as part of a retroviral or other vector, and the like.

25       Methods of administration include, e.g., intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The pharmaceutical preparations of the present invention may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together  
30 with other biologically-active agents. Administration can be systemic or local. In addition, it may be advantageous to administer the pharmaceutical preparation into the central nervous system by any suitable route, including intraventricular and intrathecal injection. Intraventricular injection may be facilitated by an intraventricular catheter attached to a

reservoir (e.g., an Ommaya reservoir). Pulmonary administration may also be employed by use of an inhaler or nebulizer, and formulation with an aerosolizing agent. It may also be desirable to administer the pharmaceutical preparation locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during 5 surgery, topical application, by injection, by means of a catheter, by means of a suppository, or by means of an implant. In a specific embodiment, administration may be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

Alternatively, pharmaceutical preparations of the invention may be delivered in a vesicle, in particular a liposome, (see, e.g., Langer, *Science* 249:1527-1533 (1990)) or via a 10 controlled release system including, e.g., a delivery pump (see, e.g., Saudek, *et al.*, *New Engl. J. Med.* 321: 574 (1989) and a semi-permeable polymeric material (see, e.g., Howard, *et al.*, *J. Neurosurg.* 71: 105 (1989)). Additionally, the controlled release system can be placed in proximity of the therapeutic target (e.g., the brain), thus requiring only a fraction of the systemic dose. See, e.g., Goodson, In: *Medical Applications of Controlled Release*, 1984 15 (CRC Press, Boca Raton, FL).

### **Screening, Diagnostic, and Therapeutic Methods**

The invention further provides methods of identifying an agent which modulate formation or stability a polypeptide complex described herein. By modulate is meant to 20 increase or decrease the rate at which the complex is assembled or dissembled, or to increase or decrease the stability of an assembled complex. Thus, an agent can be tested for its ability to disrupt a complex, or to promote formation or stability of a complex.

In one embodiment, the invention provides a method of identifying an agent that promotes disruption of a complex. The method includes providing a polypeptide complex, 25 contacting the complex with a test agent, and detecting the presence of a polypeptide displaced from the complex. The presence of displaced polypeptide indicates the disruption of the complex by the agent. In some embodiments, the complex is a human ortholog complex, as described above, which includes "bait" and "prey" proteins selected from those recited in Table 7. In other embodiments, the complex contains at least one microtubule or 30 microtubule-associated protein, as described above, and is selected from the complexes recited in Table 4. In other embodiments, the complex contains at least one heme biosynthesis protein, as described above, and is the complex recited in Table 5. In yet another embodiment, the complex contains at least one cell wall or cell wall-synthesis protein, as described above,

and is selected from the complexes recited in Table 6. Agents which disrupt complexes of the invention may present novel modulators of cell processes and pathways in which the complexes participate. For example, agents which disrupt complexes involving microtubule proteins may be selected as potential anti-fungal therapeutics.

5 Any compound or other molecule (or mixture or aggregate thereof) can be used as a test agent. In some embodiments, the agent can be a small peptide, or other small molecule produced by *e.g.*, combinatorial synthetic methods known in the art. Disruption of the complex by the test agent, *e.g.* binding of the agent to the complex, can be determined using art recognized methods, *e.g.*, detection of polypeptide using polypeptide-specific antibodies, as  
10 described above. Bound agents can alternatively be identified by comparing the relative electrophoretic mobility of complexes exposed to the test agent to the mobility of complexes that have not been exposed to the test agent.

15 Agents identified in the screening assays can be further tested for their ability to alter and/or modulate cellular functions, particularly those functions in which the complex has been implicated. These functions include, *e.g.*, control of cell-cycle progression; regulation of transcription; control of intracellular signal transduction, etc., as described in detail above.

20 In another embodiment, the invention provides methods for inhibiting the interaction of a polypeptide with a ligand, by contacting a complex of the protein and the ligand with an agent that disrupts the complex, as described above. In certain embodiments, the polypeptides are microtubule or microtubule-associated proteins, heme biosynthesis proteins, or cell wall or cell wall-synthesis proteins. In certain embodiments, the ligand is an interacting polypeptide, and the polypeptide and ligands are selected from those recited in Tables 4-6. Inhibition of complex formation allows for modulation of cellular functions and pathways in which the targeted complexes participate.

25 In another embodiment, the invention provides a method for identifying a polypeptide complex in a subject. The method includes the steps of providing a biological sample from the subject, detecting, if present, the level of polypeptide complex. In some embodiments, the complex includes a first polypeptide (a "bait" polypeptide) selected from the polypeptides recited in Table 7, column 2, and a second polypeptide ("prey" polypeptide) selected from the polypeptides recited in Table 7, column 6. Any suitable biological sample potentially containing the complex may be employed, *e.g.* blood, urine, cerebral-spinal fluid, plasma, etc. Complexes may be detected by, *e.g.*, using complex-specific antibodies as described above.

The method provides for diagnostic screening, including in the clinical setting, using, e.g., the kits described above.

In still another embodiment, the present invention provides methods for detecting a polypeptide in a biological sample, by providing a biological sample containing the 5 polypeptide, contacting the sample with a corresponding polypeptide to form a complex under suitable conditions, and detecting the presence of the complex. A complex will form if the sample does, indeed, contain the first polypeptide. In some embodiments, the polypeptide being detecting is a "prey" protein selected from the polypeptides recited in Table 7, column 6, and is detected by complexing with the corresponding "bait" protein recited in Table 7, 10 column 2. Conversely, in other embodiments the polypeptide being detected is the "bait" protein. Alternatively, a yeast "bait" or "prey" ortholog may be employed to form a chimeric complex with the polypeptide in the biological sample.

In still another embodiment, the invention provides methods for removing a first polypeptide from a biological sample by contacting the biological sample with the 15 corresponding second peptide to form a complex under conditions suitable for such formation. The complex is then removed from the sample, effectively removing the first polypeptide. As with the methods of detecting polypeptide described above, the polypeptide being removed may be either a "bait" or "prey" protein, and the second corresponding polypeptide used to remove it may be either a yeast or human ortholog polypeptide.

20 Methods of determining altered expression of a polypeptide in a subject, e.g. for diagnostic purposes, are also provided by the invention. Altered expression of proteins involved in cell processes and pathways can lead to deleterious effects in the subject. Altered expression of a polypeptide in a given pathway leads to altered formation of complexes which include the polypeptide, hence providing a means for indirect detection of the polypeptide 25 level. The method involves providing a biological sample from a subject, measuring the level of a polypeptide complex of the invention in the sample, and comparing the level to the level of complex in a reference sample having known polypeptide expression. A higher or lower complex level in the sample versus the reference indicates altered expression of either of the polypeptides that forms the complex. The detection of altered expression of a polypeptide can 30 be used to diagnose a given disease state, and or used to identify a subject with a predisposition for a disease state. Any suitable reference sample may be employed, but preferably the test sample and the reference sample are derived from the same medium, e.g. both are urine, etc.

The reference sample should be suitably representative of the level polypeptide expressed in a control population.

In a certain embodiment, the polypeptide complex contains a "bait" polypeptide selected from the polypeptides recited in Table 7, column 2, and a "prey" polypeptide selected 5 from the polypeptides recited in Table 7, column 6.

The invention further provides methods for treating or preventing a disease or disorder involving altered levels of a polypeptide complex, or polypeptide, disclosed herein, by administering to a subject a therapeutically-effective amount of at least one molecule that modulates the function of the complex. As discussed above, altered levels of polypeptide. 10 complexes described herein may be implicated in disease states resulting from a deviation in normal function of the pathway in which a complex is implicated. For example, altered levels of the observed complex between YGR010Wp and YLR328Wp may be implicated in disruptions in arginine metabolism, leading to retinal atrophy, for example. In subjects with a deleteriously high level of complex, modulation may consist, for example, by administering an 15 agent which disrupts the complex, or an agent which does not disrupt, but down-regulates, the functional activity of the complex. Alternatively, modulation in subjects with a deleteriously low level of complex may be achieved by pharmaceutical administration of complex, constituent polypeptide, or an agent which up-regulates the functional activity of complex. Pharmaceutical preparations suitable for administration of complex are described above.

20 In one embodiment, a disease or disorder involving altered levels of a polypeptide selected from the polypeptides recited in Table 7, column 2 or the corresponding polypeptides in column 4, is treated by administering a molecule that modulates the function of the polypeptide. In certain embodiments, the modulating molecule is the corresponding 25 polypeptide, *e.g.* administering a "prey" protein corresponding to a "bait" protein modulates the latter by forming a complex with it.

The details of one or more embodiments of the invention are set forth in the description above. Although any methods and materials similar or equivalent to those described herein can be used in the practice of the present invention, the preferred methods and materials are now described. For example, additional interactions can be identified using other two-hybrid 30 systems (*i.e.* using a LexA binding domain fusion or *HIS3* as a reporter gene), including variables such as different protein domains or genomic activation domain libraries. Other features, objects, and advantages of the invention will be apparent from the description and from the claims.

The following examples are presented in order to more fully illustrate the preferred embodiments of the invention. These examples should in no way be construed as limiting the scope of the invention, as defined by the appended claims.

## 5 EXAMPLE 1—CLONING OF *S. CEREVIAE* OPEN-READING FRAMES

6144 potential yeast open-reading frames (ORFs) have been previously described. See Goffeau *et al.*, *supra*. These ORFs were amplified by PCR as full-length fragments, and each fragment was fused to sequences encoding the Gal4 DNA binding domain and the Gal4 activation domain by gap-repair cloning into the vectors pOBD2 and pOAD. PCR amplified products of the 6144 yeast ORFs were made by amplification of yeast cDNA using 70 oligonucleotide primers to allow recombination with centromeric plasmids pOBD2 and pOAD. See Hudson *et al.*, *Genome Res* 7: 1169 (1997). The yeast strains used were YULH (*MATα ura3-52 trp1 lys2 his3 leu2 gal4 gal80 GAL1-URA3 GAL1-LacZ*) for the Gal4 binding domain fusion in pOBD2 and N106r (*MATα ura3-52 his3 ade2 trp1 leu2 gal4 gal80 cyh2 lys2::GAL1-HIS3 ura3::GAL1-LacZ*) for the Gal4 AD fusion in pOAD. Yeast transformations were performed in a 96-well format using the lithium acetate procedure. See Ito *et al.*, *J. Bacteriol.* 153: 163 (1983). Five µl from individual transformations were grown on selective media lacking leucine (Sc-Leu) or tryptophan (Sc-Trp) for two days and grown at 30°C. Patches of transformants were manually transferred into individual wells on micro-assay plates, to generate 64 barcoded 96-well plates for further use.

Of the 6144 ORFs, 5345 (87%) were successfully cloned into both plasmids (Table 1). Transformants from the Gal4 activation domain array were pooled to form an activation domain library. As yeast strains of opposite mating type were used to generate the two arrays, each binding domain fusion transformant was mated in duplicate to the activation domain library, and diploid cells that expressed interacting pairs were selected. Mating reactions were performed on 96-well filter plates (Millipore MAHV S45) by mixing  $10^7$  *MATα* cells (Gal4 binding domain fusion) with  $5 \times 10^6$  *MATα* cells (activation domain library) from liquid cultures in complete media (YPAD). After filtration, the 96-well filter plates were incubated overnight at 30°C on rectangular YPAD solid media plates. Cells were collected from each filter with sterile water and the diploids containing potential interactors were selected on media lacking uracil and simultaneously screened by the addition of X-gal by incubating 4 days at 30°C. Each mating generated  $5 \times 10^5$  to  $10^6$  diploids per well, and was performed in

duplicate to insure the reproducibility of the results. Up to 12 blue colonies were picked per mating and submitted for PCR and sequencing. A total of 8676 blue colonies were picked from the screen, 6909 (80%) passed PCR, sequencing, vector trimming, and annotation quality control, and 6215 (72%) passed interaction quality control.

5 To conduct transformation and mating reactions on such a large scale in a timely fashion, 96-well assay plates and a semi-automated Zymark® work station were used throughout the cloning and screening procedures. Sample handling and manipulation during the screens were tracked by computer, and data analysis was carried out using web-based software developed at CuraGen (GeneScape®). The final product of the screening process  
10 was a collection of 96-well plates of diploid clones. The activation domain fusion plasmids were sequenced to identify the yeast ORF. The resulting sequences were compared to the yeast sequence database using Blast2. *See* Altschul *et al.*, *J. Mol. Biol.* 215: 403 (1990). Using these results, a list of interactors was obtained, as discussed above (*see* Table 3).

15 Results from this screen were also compared with a compilation of previously described interactions. Thirty-one protein pairs identified in the present screen were previously reported as two-hybrid interactions, and an additional 18 pairs confirmed interactions previously identified by biochemical assays (co-immunoprecipitation, copurification, affinity column). *See* MIPS Yeast Genome Database (MYGD) Functional Catalogue, *supra.*; Mewes *et al.*, *supra.*; YPD™ information available at  
20 [www.proteome.com/YPDhome.html](http://www.proteome.com/YPDhome.html). Thus, 49 out of the 692 interactions identified in this screen overlap the approximately 700 interactions in *S. cerevisiae* reported in the literature. *See id.*

25 The limited overlap between the results described herein and the literature (7%) can be attributed to specifics of the screen: the exclusive use of full-length proteins as both binding and activation domain fusions and the version of the two-hybrid system used, which includes Gal4 as the binding domain fusion protein, centromeric plasmids, and a stringent reporter gene (*URA3*). Each of these components can affect the sensitivity of the assay. *See* Legrain *et al.*, *Nucl. Acid. Res.* 22: 3241 (1994).

**CLAIMS****WE CLAIM:**

- 5      1. A purified complex comprising a first polypeptide and a second polypeptide, wherein  
said first polypeptide comprises an amino acid sequence of a polypeptide selected from  
the group consisting of the polypeptides recited in Table 3, column 1, and wherein said second  
polypeptide comprises an amino acid sequence of the corresponding polypeptide recited in  
Table 3, column 5; or
- 10     10    said first polypeptide comprises an amino acid sequence of a polypeptide selected from  
the group consisting of the polypeptides recited in Table 7, column 2, and wherein said second  
polypeptide comprises the amino acid sequence of the corresponding polypeptide recited in  
Table 7, column 6; or  
15     15    said first and second polypeptide comprise the amino acid sequences of a first  
polypeptide-second polypeptide selected from the group consisting of APG7-AUT7,  
DUO1-BIM1, BUB3-MAD3, KAR4-MUM2, CLN3-MAD3, EBS1-MAD2, MSB2-MAD2,  
MSB2-MAD3, NUP157-MAD2, SAP4-MAD2, SAP4-MAD3, SIN4-MAD2, SIN4-MAD3,  
YDR214W-MAD2, YNL218W-MAD2, MCM16-MCM22, CYP2-JSN1, SPC34-JSN1,  
YIL065C-JSN1, YLR392C-JSN1, SED1-HEM13, CDC11-SPR28, YFR042W-KRE6,  
20     20    YDR482C-SCW11, SMI1-BAS1, and WSC3-PEX14.
- 25     2. The complex of claim 1, wherein said first polypeptide is selected from the group  
consisting of the polypeptides recited in Table 3, column 1, and wherein said second  
polypeptide is the corresponding polypeptide recited in Table 3, column 5.
- 30     25    3. The complex of claim 1, wherein said first polypeptide is labeled.
- 35     30    4. The complex of claim 1, wherein said second polypeptide is labeled.
- 40     35    5. The complex of claim 3, wherein said second polypeptide is labeled.
- 45     40    6. The complex of claim 1, wherein said first polypeptide is selected from the group of  
polypeptides recited in Table 3, column 1, which are denoted as ProPair 1a-128a, and wherein  
said second polypeptide is the corresponding polypeptide selected from the group consisting  
of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 1b-128b.

7. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 129a-140a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 129b-140b.
- 5
8. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 141a-144a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 141b-141b.
- 10
9. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 145a-154a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 145b-154b.
- 15
- 20 10. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 155a-170a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 155b-170b.
- 25
11. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 171a-177a, and wherein said second polypeptide is the corresponding polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 171b-177b.
- 30
12. The complex of claim 1, wherein said first polypeptide is selected from the group of polypeptides recited in Table 3, column 1, which are denoted as ProPair 178a-194a, and wherein said second polypeptide is the corresponding polypeptide selected from the group

consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 178b-194b.

13. The complex of claim 1, wherein said first polypeptide is selected from the group of  
5 polypeptides recited in Table 3, column 1, which are denoted as ProPair 195a-310a, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group  
consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair  
195b-310b.

10 14. The complex of claim 1, wherein said first polypeptide is selected from the group of  
polypeptides recited in Table 3, column 1, which are denoted as ProPair 311a-351a, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group  
consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair  
311b-351b.

15 15. The complex of claim 1, wherein said first polypeptide is selected from the group of  
polypeptides recited in Table 3, column 1, which are denoted as ProPair 352a-367a, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group  
consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair  
20 352b-367b.

16. The complex of claim 1, wherein said first polypeptide is the polypeptide recited in  
Table 3, column 1, which is denoted as ProPair 368a, and wherein said second polypeptide is  
the corresponding polypeptide recited in Table 3, column 5, which is denoted as ProPair 368b.

25 17. The complex of claim 1, wherein said first polypeptide is selected from the group of  
polypeptides recited in Table 3, column 1, which are denoted as ProPair 369a-374aa, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group  
consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair  
30 369b-374b.

18. The complex of claim 1, wherein said first polypeptide is selected from the group of  
polypeptides recited in Table 3, column 1, which are denoted as ProPair 375a-431a, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group

consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair 375b-431b.

19. The complex of claim 1, wherein said first polypeptide is selected from the group of  
5 polypeptides recited in Table 3, column 1, which are denoted as ProPair 432a-440a, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group  
consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair  
432b-440b.

10 20. The complex of claim 1, wherein said first polypeptide is selected from the group of  
polypeptides recited in Table 3, column 1, which are denoted as ProPair 441a-580a, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group  
consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair  
441b-580b.

15 21. The complex of claim 1, wherein said first polypeptide is selected from the group of  
polypeptides recited in Table 3, column 1, which are denoted as ProPair 581a-692a, and  
wherein said second polypeptide is the corresponding polypeptide selected from the group  
consisting of the polypeptides recited in Table 3, column 5, which are denoted as ProPair  
20 581b-692b.

22. The complex of claim 1, wherein said first and second polypeptide comprise the amino  
acid sequences of a first polypeptide-second polypeptide selected from the group consisting of  
APG7-AUT7, DUO1-BIM1, BUB3-MAD3, KAR4-MUM2, CLN3-MAD3, EBS1-MAD2,  
25 MSB2-MAD2, MSB2-MAD3, NUP157-MAD2, SAP4-MAD2, SAP4-MAD3, SIN4-MAD2,  
SIN4-MAD3, YDR214W-MAD2, YNL218W-MAD2, MCM16-MCM22, CYP2-JSN1,  
SPC34-JSN1, YIL065C-JSN1, YLR392C-JSN1, SED1-HEM13, CDC11-SPR28,  
YFR042W-KRE6, YDR482C-SCW11, SMI1-BAS1, and WSC3-PEX14.

30 23. The complex of claim 1, wherein said first polypeptide comprises an amino acid  
sequence of a polypeptide selected from the group consisting of the polypeptides recited in  
Table 7, column 2, and wherein said second polypeptide comprises the amino acid sequence of  
the corresponding polypeptide recited in Table 7, column 6.

24. The complex of claim 1, wherein said first polypeptide is selected from the group consisting of the polypeptides recited in Table 7, column 2, and wherein said second polypeptide is the corresponding polypeptide recited in Table 7, column 6.

5 25. A purified complex comprising a first polypeptide and a second polypeptide, wherein said first polypeptide comprises a region of amino acids of a polypeptide selected from the group consisting of the polypeptides recited in Table 3, column 1 sufficient to allow said first polypeptide to bind said second polypeptide, and wherein said second polypeptide comprises a region of amino acids of the corresponding polypeptide recited in Table 3, column 10 5 sufficient to bind said first polypeptide.

26. A chimeric polypeptide comprising six or more amino acids of the first polypeptide of claim 1 covalently linked to six or more amino acids of the second polypeptide of claim 1.

15 27. A nucleic acid encoding the chimeric polypeptide of claim 26.

28. A vector comprising the nucleic acid of claim 27.

29. A cell comprising the vector of claim 28.

20 30. An antibody which specifically binds the complex of claim 1.

31. The antibody of claim 30, wherein said antibody binds to the complex of claim 1 with higher affinity than it binds to said first or second polypeptide when said polypeptides are not 25 complexed.

32. A pharmaceutical composition comprising the complex of claim 1.

33. A kit comprising a reagent which can specifically detect the complex of claim 1.

30 34. The kit of claim 33, wherein said reagent is selected from the group consisting of an antibody specific for said complex, an antibody specific for said first polypeptide, and an antibody specific for said second polypeptide.

35. A method of identifying an agent which disrupts a polypeptide complex, the method comprising:

- (a) providing the complex of claim 1;
- (b) contacting the complex with a test agent; and
- 5 (c) detecting the presence of a polypeptide displaced from said complex,  
wherein the presence of displaced polypeptide indicates said agent disrupts said complex.

10 36. A method for identifying an agent which disrupts a polypeptide complex comprising at least one microtubule/microtubule-associated protein, heme biosynthesis protein, or cell wall/cell-wall synthesis protein, the method comprising:

- (a) providing the complex of claim 22;
- (b) contacting said complex with a test agent; and
- (c) detecting the presence of a polypeptide displaced from said complex,  
15 wherein the presence of displaced polypeptide indicates said agent disrupts said complex.

20 37. A method for inhibiting interaction of a microtubule or microtubule-associated protein, with a ligand, the method comprising:

- contacting a complex comprising said protein and said ligand with an agent that disrupts said complex, wherein said complex is selected from the group consisting of APG7-AUT7, DUO1-BIM1, BUB3-MAD3, KAR4-MUM2, CLN3-MAD3, EBS1-MAD2, MSB2-MAD2, MSB2-MAD3, NUP157-MAD2, SAP4-MAD2, SAP4-MAD3, SIN4-MAD2, SIN4-MAD3, YDR214W-MAD2, YNL218W-MAD2,  
25 MCM16-MCM22, CYP2-JSN1, SPC34-JSN1, YIL065C-JSN1, and YLR392C-JSN1, thereby inhibiting interaction of said protein with said ligand.

30 38. A method for inhibiting interaction of a heme biosynthesis protein with a ligand, the method comprising:

- contacting a complex comprising said protein and said ligand with an agent that disrupts said complex, wherein said complex comprises SED1-HEM13, thereby inhibiting interaction of said protein with said ligand.

39. A method for inhibiting interaction of a cell wall or cell wall-synthesis protein with a ligand, said method comprising the step of:

5 contacting a complex comprising said protein and said ligand with an agent that disrupts said complex, wherein said complex is selected from the group consisting of CDC11-SPR28, YFR042W-KRE6, YDR482C-SCW11, SMI1-BAS1, and WSC3-PEX14.

thereby inhibiting interaction of said protein with said ligand.

10 40. A method of identifying a polypeptide complex in a subject, the method comprising:  
(a) providing a biological sample from said subject; and  
(b) detecting, if present, the polypeptide complex of claim 1 in said sample,  
thereby identifying said complex.

15 41. A method of detecting a polypeptide in a biological sample, the method comprising:

(a) providing a biological sample comprising the first polypeptide of claim 1;

(b) contacting said biological sample with the second polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptides; and

20 (c) detecting the presence of a complex of said first and second polypeptide, wherein the presence of said complex indicates the presence of said first polypeptide in said sample.

42. A method of detecting a polypeptide in a biological sample, the method comprising:

25 (a) providing a biological sample comprising the second polypeptide of claim 1;

(b) contacting said biological sample with the first polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptides; and

(c) detecting the presence of a complex of said first and second polypeptide,

30 wherein the presence of said complex indicates the presence of said second polypeptide in said sample.

43. A method of removing a polypeptide from a biological sample, the method comprising:
- (a) providing a biological sample comprising the first polypeptide of claim 1;
  - (b) contacting said biological sample with the second polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptide; and
  - (c) removing said complex from said sample,
- thereby removing said first polypeptide from said sample.
- 10 44. A method of determining altered expression of a polypeptide in a subject, the method comprising:
- (a) providing a biological sample from said subject,
  - (b) measuring the level of the complex of claim 1 in said sample; and
  - (c) comparing the level of said complex from step (b) to the level of said complex in a reference sample whose level of the complex of claim 1 is known,
- 15 thereby determining whether said subject has altered expression of said first or second polypeptide.
45. A method of treating or preventing a disease or disorder involving altered levels of the complex of claim 1, the method comprising:
- 20 administering a therapeutically-effective amount of least one molecule that modulates the function of said complex to a subject in need thereof.

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(54) Title: PROTEIN-PROTEIN FROM S. CEREVISIAE AND METHODS OF USING SAME

(57) Abstract: The invention provides complexes of at least two polypeptides from the yeast *S. cerevisiae* and methods of using the same. Purified complexes of two polypeptides are provided, including chimeric complexes, and chimeric polypeptides and complexes thereof are also provided, as are nucleic acids encoding chimeric polypeptides and vectors and cells containing the same. Also provided are methods of identifying agents that disrupt polypeptide complexes, methods of identifying complex or polypeptide in a sample, and for removing the same, methods of determining altered expression of a polypeptide in a subject and methods of treating/preventing disorders involving altered levels of complex or polypeptide.

WO 00/60066 A1

**INTERNATIONAL SEARCH REPORT**

Information on patent family members

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Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 0046406	A 10-08-2000	NONE		
WO 9935256	A 15-07-1999	AU 1778099	A	26-07-1999

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-45

Present claims 1-45 relate to an extremely large number of possible compounds and thereon based methods. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found, however, for only a very small proportion of the compounds and pertinent methods claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Consequently, the search has been carried out for those parts of the claims which appear to be supported and disclosed, namely those parts relating to the use of double-hybrid technique for screening of *S. cerevisiae* and thereby detected proteins. This method is not claimed per se, but is the basis of the present application. Moreover the subject matter of all claims was considered to be so speculative in scope that no more refined search was deemed to be possible.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 00/08399

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO 99 35256 A (INSTITUT PASTEUR & AFFIMETRIX) 15 July 1999 (1999-07-15) the whole document ---	1-45
P, X	A FLORES ET AL.: "A protein-protein interaction map of yeast RNA polymerase III" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA., vol. 96, no. 14, 6 July 1999 (1999-07-06), pages 7815-7820, XP002146712 NATIONAL ACADEMY OF SCIENCE. WASHINGTON., US ISSN: 0027-8424 cited in the application the whole document ---	1-45
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## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 00/08399

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	L WODICKA ET AL.: "Genome-wide expression monitoring in <i>Saccharomyces cerevisiae</i> " NATURE BIOTECHNOLOGY., vol. 15, no. 12, December 1997 (1997-12), pages 1359-1367, XP002100297 NATURE PUBLISHING., US ISSN: 1087-0156 the whole document ---	1-45
X	N LECRENIER ET AL.: "Two-hybrid systematic screening of the yeast proteome" BIOESSAYS, vol. 20, no. 1, January 1998 (1998-01), pages 1-5, XP002100659 CAMBRIDGE, GB ISSN: 0265-9247 the whole document ---	1-45
X	C BENDIXEN ET AL.: "A yeast mating-selection for detection of protein-protein interactions" NUCLEIC ACIDS RESEARCH., vol. 22, no. 9, 1994, pages 1778-1779, XP002004038 OXFORD UNIVERSITY PRESS, SURREY., GB ISSN: 0305-1048 the whole document ---	1-45
X	Y LUO ET AL.: "Cloning and analysis of DNA-binding proteins by yeast one-hybrid and one-two-hybrid systems" BIOTECHNIQUES., vol. 20, no. 4, April 1996 (1996-04), pages 564-568, XP002146710 EATON PUBLISHING, NATICK., US ISSN: 0736-6205 the whole document ---	1-45
X	R J CHO ET AL.: "Parallel analysis of genetic selections using whole genome oligonucleotide arrays" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA., vol. 95, no. 7, 31 March 1998 (1998-03-31), pages 3752-3757, XP002146711 NATIONAL ACADEMY OF SCIENCE. WASHINGTON., US ISSN: 0027-8424 the whole document ---	1-45
E	WO 00 46406 A (ALPHAGENE INC.) 10 August 2000 (2000-08-10) the whole document ---	1-45
	-/-	

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 00/08399

**A. CLASSIFICATION OF SUBJECT MATTER**  
 IPC 7 C12N15/10 C07K14/395 G01N33/68 C07K16/16

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)  
 IPC 7 C12N C07K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

CHEM ABS Data, BIOSIS, WPI Data

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>M FROMONT-RACINE ET AL.: "Toward a functional analysis of the yeast genome through exhaustive two-hybrid screens"  <b>NATURE GENETICS</b>,          vol. 16, no. 7, 16 July 1997 (1997-07-16),          pages 277-282, XP000770741  <b>NATURE AMERICA, NEW YORK., US</b>          ISSN: 1061-4036          cited in the application          the whole document</p> <p style="text-align: center;">----</p> <p style="text-align: center;">-/--</p>	1-45

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

\* Special categories of cited documents :

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Date of the actual completion of the international search

Date of mailing of the international search report

6 September 2000

19/09/2000

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